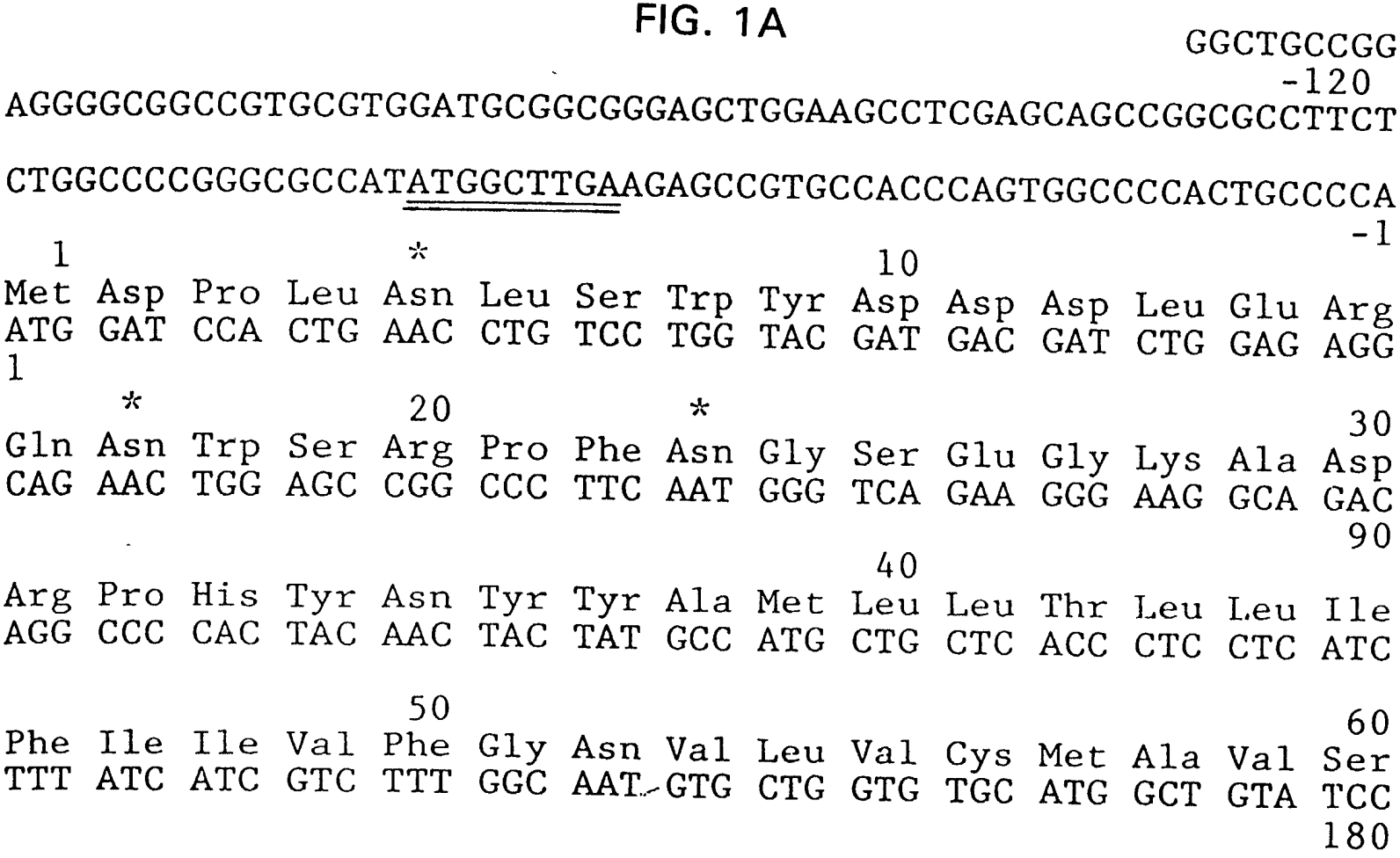
FIG. 1A


GGCTGCCGG
-120
AGGGGCGGCCGTGCGTGGATGCGGCGGGAGCTGGAAGCCTCGAGCAGCCGGCGCCTTCT
CTGGCCCCGGGCGCCATATGGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCCA
-1
1
*
10
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
ATG GAT CCA CTG AAC CTG TCC TGG TAC GAT GAC GAT CTG GAG AGG
1
*
20
*
30
Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GGG AAG GCA GAC
90
40
Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile
AGG CCC CAC TAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC
50
60
Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
TTT ATC ATC GTC TTT GGC AAT GTG CTG GTG TGC ATG GCT GTA TCC
180

```
                                                    70
Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser
GCA GAG AAG GCT TTG CAG ACC ACC ACC AAC TAC TTG ATA GTC AGC

                    80                                  90
Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val Met Pro Trp
CTT GCT GTG GCT GAT CTT CTG GTG GCC ACA CTG GTA ATG CCG TGG

                                                       270
                                        100
Val Val Tyr Leu Glu Val Val Gly Glu Trp Lys Phe Ser Arg Ile
GTT GTC TAC CTG GAG GTG GTG GGT GAG TGG AAA TTC AGC AGG ATT

                    110                                120
His Cys Asp Ile Phe Val Thr Leu Asp Val Met Met Cys Thr Ala
CAC TGT GAC ATC TTT GTC ACT CTG GAT GTC ATG ATG TGC ACA GCA

                                                       360
                                    130
Ser Ile Leu Asn Leu Cys Ala Ile Ser Ile Asp Arg Tyr Thr Ala
AGC ATC CTG AAC CTG TGT GCC ATC AGC ATT GAC AGG TAC ACA GCT

                    140                                150
Val Ala Met Pro Met Leu Tyr Asn Thr Arg Tyr Ser Ser Lys Arg
GTG GCA ATG CCC ATG CTG TAT AAC ACA CGC TAC AGC TCC AAG CGC

                                                       450
```

FIG. 1B

```
                                                    160
Arg Val Thr Val Met Ile Ala Ile Val Trp Val Leu Ser Phe Thr
CGA GTT ACT GTC ATG ATT GCC ATT GTC TGG GTC CTG TCC TTC ACC

                170                                     180
Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn Thr Asp Gln Asn
ATC TCC TGC CCA CTG CTC TTC GGA CTC AAC AAT ACA GAC CAG AAT

                                                        540
                                    190
Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr Ser Ser Ile
GAG TGT ATC ATT GCC AAC CCT GCC TTT GTG GTC TAC TCC TCC ATT

                200                                     210
Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val Tyr Ile
GTC TCA TTC TAC GTG CCC TTC ATC GTC ACT CTG CTG GTC TAT ATC

                                                        630
                                220
Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn Thr
AAA ATC TAC ATC GTC CTC CGG AAG CGC CGG AAG CGG GTC AAC ACC

                230                                     240
Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu
AAG CGC AGC AGT CGA GCT TTC AGA GCC AAC CTG AAG ACA CCA CTC

                                                        720
```

FIG. 1C

```
Lys Asp Ala Ala Arg Arg Ala Gln Glu                    250
AAG GAT GCT GCC CGC CGA GCT CAG GAG Leu Glu Met Glu Met Leu
AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG

                    260
Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro
TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC CCT
                                                       270
                                                       810
Pro Ser His His Gln Leu Thr Leu Pro                    280
CCC AGT CAC CAC CAG CTC ACT CTC CCT Asp Pro Ser His His Gly
CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC

                    290
Leu His Ser Asn Pro Asp Ser Pro Ala Lys Pro Gly Lys Asn Gly
CTA CAT AGC AAC CCT GAC AGT CCT GCC AAA CCA GAG AAG AAT GGG
                                                       300
                                                       900
His Ala Lys Ile Val Asn Pro Arg Ile                    310
CAC GCC AAG ATT GTC AAT CCC AGG ATT Ala Lys Phe Phe Glu Ile
CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG TTC TTT GAG ATC

                    320
Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met
CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG ATG
                                                       330
                                                       990
```

FIG. 1D

```
Ser Arg Arg Lys Leu Ser Gln Gln Lys                    340
AGC CGC AGA AAG CTC TCC CAG CAG AAG GAG AAG AAA GCC ACT CAG

                    350
Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro
                                                       360
ATG CTT GCC ATT GTT CTC GGT GTG TTC ATC ATC TGC TGG CTG CCC

                                                      1080
Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile
                                370
TTC TTC ATC ACG CAC ATC CTG AAT ATA CAC TGT GAT TGC AAC ATC

                    380
Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn
                                                       390
CCA CCA GTC CTC TAC AGC GCC TTC ACA TGG CTG GGC TAT GTC AAC

                                                      1170
Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe
                                400
AGT GCC GTC AAC CCC ATC ATC TAC ACC ACC TTC AAC ATC GAG TTC

                    410
Arg Lys Ala Phe Met Lys Ile Leu His Cys
                                415
CGC AAG GCC TTC ATG AAG ATC TTG CAC TGC TGAGTCTGCCCCTTGCCTG

                                                      1264
```

FIG. 1E

CACAGCAGCTGCTTCCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG

TGGGCAGAAAGGCCCAGATGAACTTGGCCTTCTCTCGACCCTGCAGGCCCTGCAGTGTTA
1383

GCTTGGCTCGATGCCCCTCTCTGCCCACACACCCTCATCCTGCCAGGGTAGGGCCAGGG

AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC
1502

CCCTCTCATATCCAGACCCTGTCTCCTTGGCACCAAAGATGCAGCGGCCTTCCTTGACC

TTCCTCTTGGGCACAGAAACTAGCTCAGTGGTCGAGCACACCCTGATCGCTGGCTTGGCC
1621

TGGCCCTTGCTTGCCTGTGCCGGATCAGGTGGTGGGAGGGAGCGACACGTTCTTACTTT

ATAGGAACCACATAGGAAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTCAGG
1740

AGACACACATAAACACCAGGTAGCTCCATGGACCCCAGAGAAACTGAGGCTGAAAAATC

TGTTTTCCACTCCAACTCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG
1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAAACAACTCTA

ATCCTCAAGGGCCCCAAGAGAATCTGTAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT

1978

CCAATCCACTCCACCACTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG

CTGGCCAGTCAGGCCTTGGACCAGTGTTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT

2097

CTTTGGGGCTGGGGGGGTTGTTAACATCGTCTCTCTTCCATATCTCTTCCTTCCCAGTG

CCTCTGCCTTAGAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTGGGCCTGG

2216

CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAACAT

CACTATACCTGTACCAAAACTAATAAAACCTTGACAAGAGTCAAAAAAAAAAAA

2317

FIG. 1G

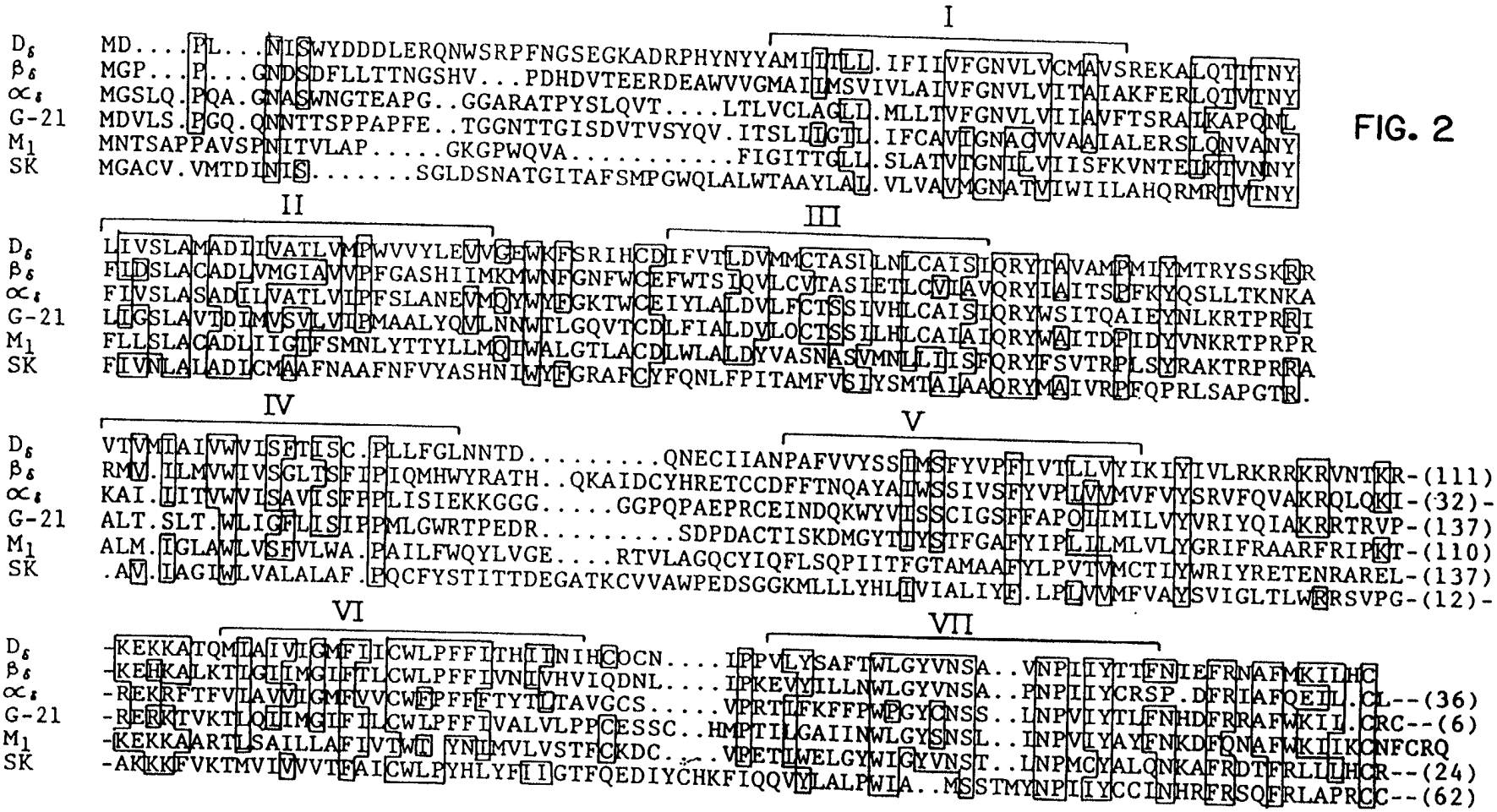


FIG. 2

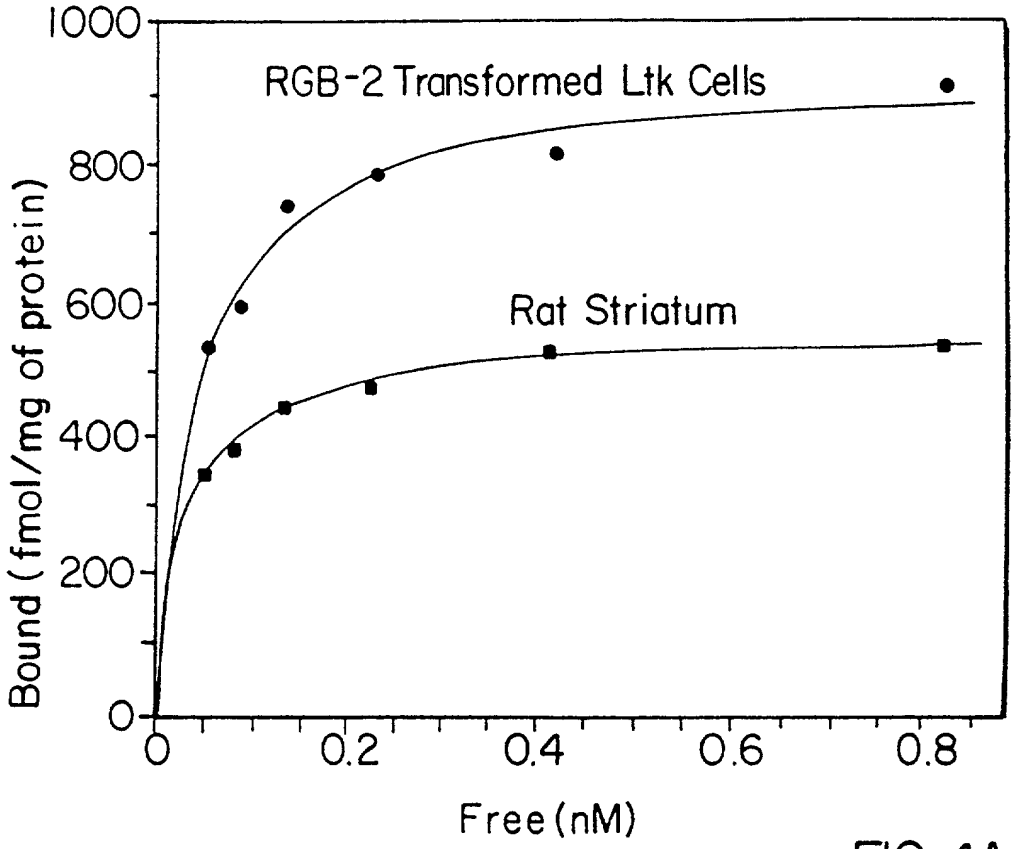


FIG.4A-1

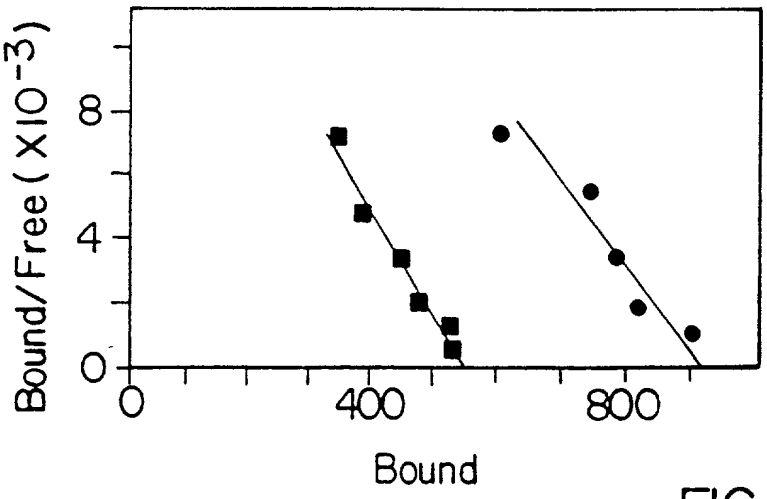
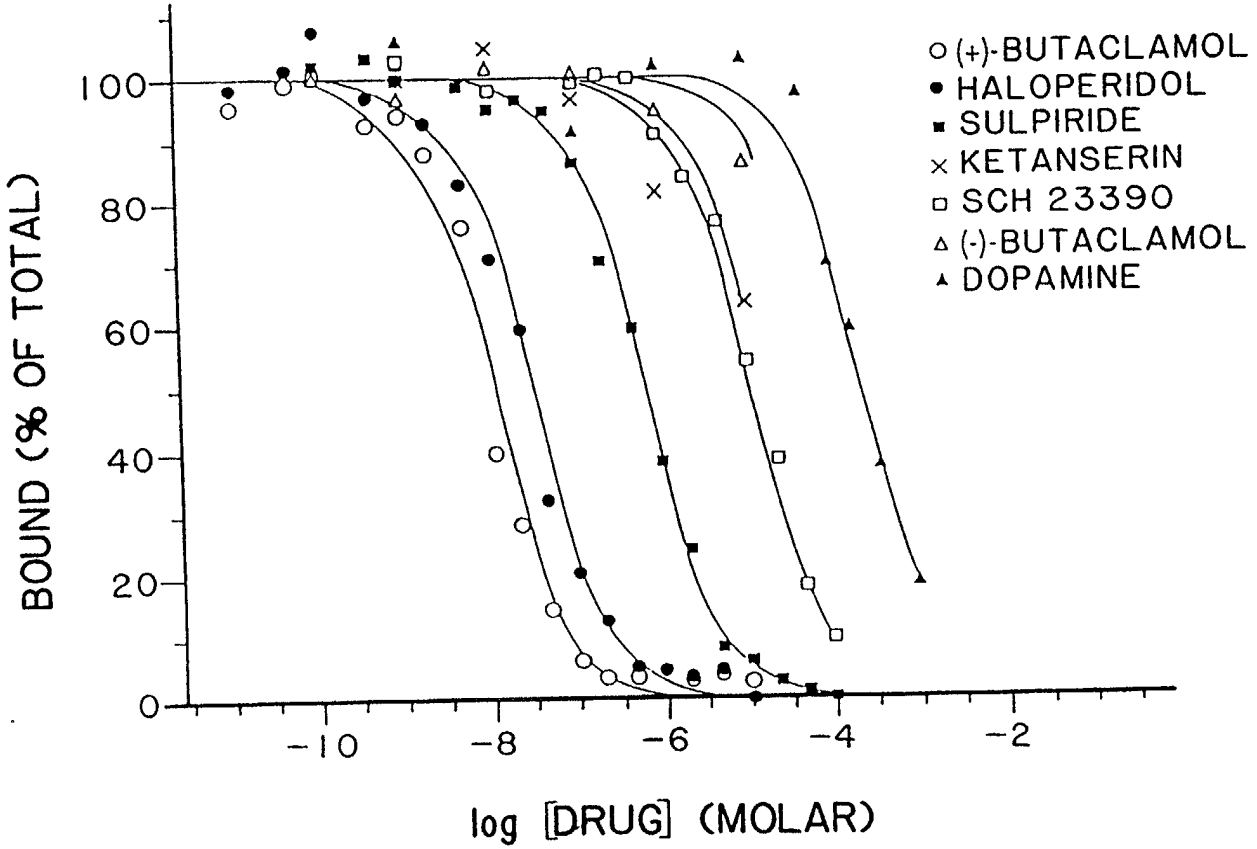


FIG.4A-2

FIG. 4B



DRUG	Ki (nM)	
	RGB-2	
	Transformed Ltk-Cells	Rat Striatum
(+)-Butaclamol	0.83	1.0
(-)-Butaclamol	>1,000	>1,000
Haloperidol	3.0	5.3
Dopamine + GTP	17,000	6,300
Sulpiride		
high affinity	80	67 (87%)
low affinity	---	>10,000 (13%)
SCH 23390		
high affinity	---	35 (16%)
low affinity	1,000	780 (84%)
Ketanserin		
high affinity	---	27 (25%)
low affinity	>1,000	>1,000 (75%)

FIG. 4C

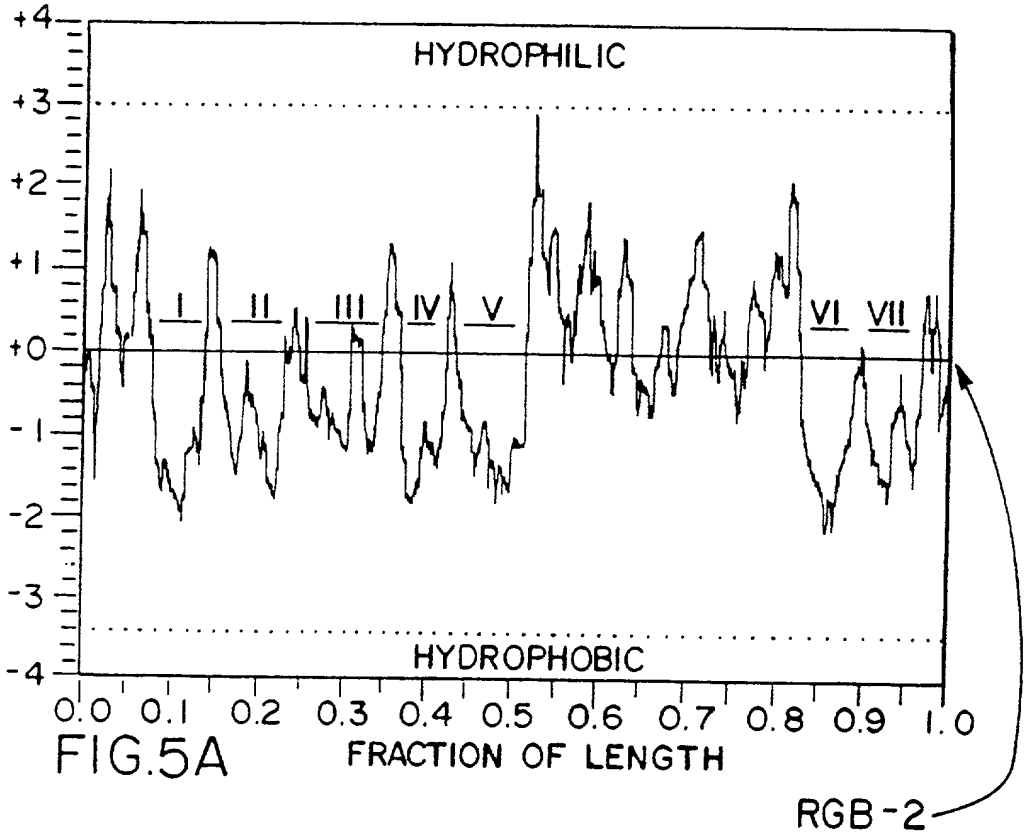

+4
+3
+2
+1
+0
-1
-2
-3
-4
HYDROPHILIC
HYDROPHOBIC
I
II
III
IV
V
VI
VII
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
FRACTION OF LENGTH
RGB-2

FIG.5A

FIG.5B

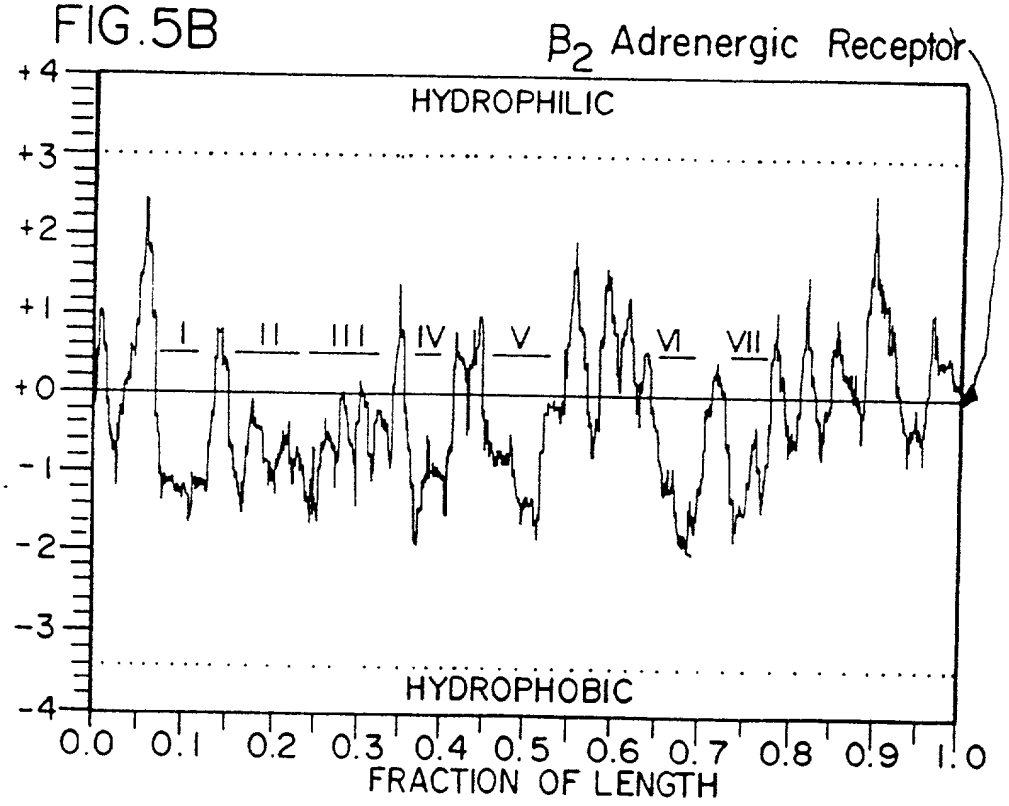
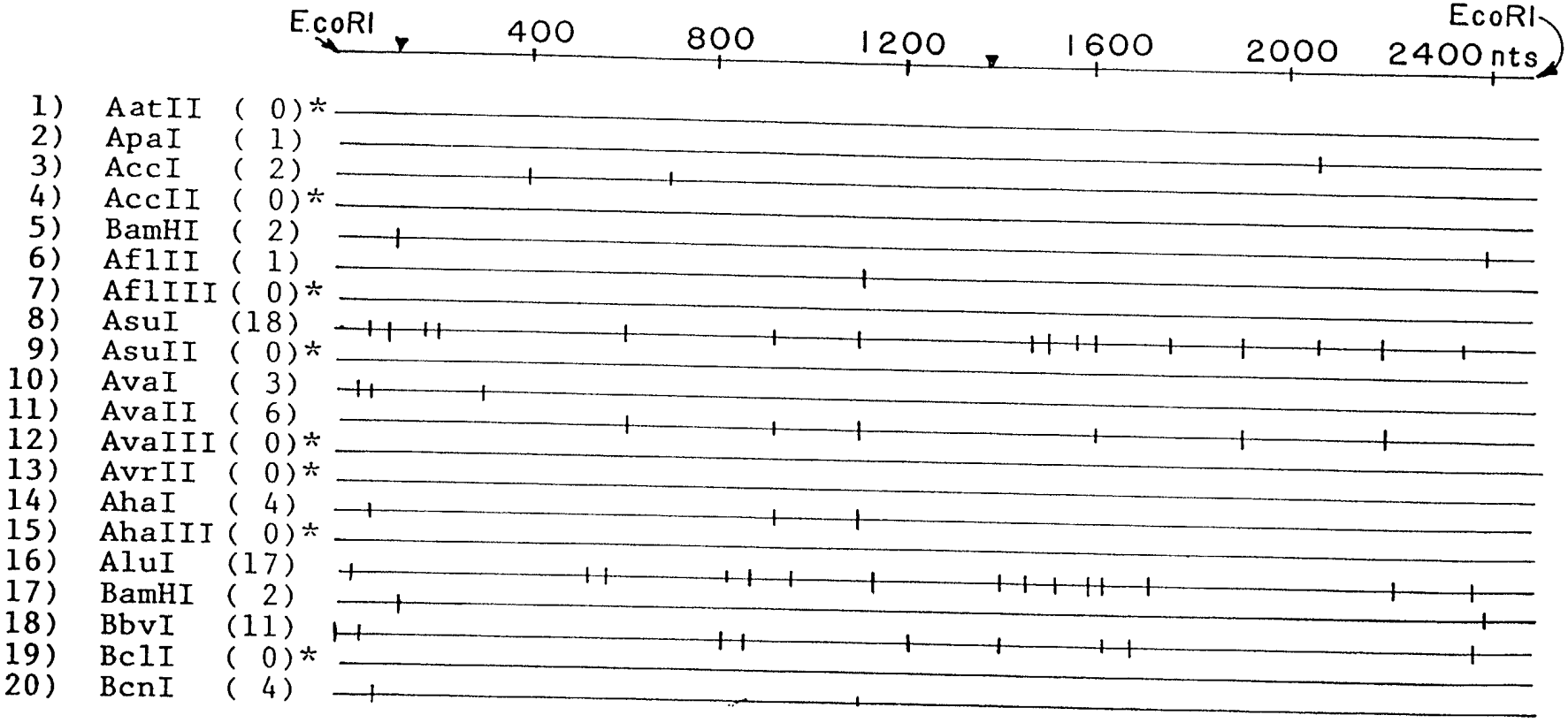

β_2 Adrenergic Receptor
+4
+3
+2
+1
+0
-1
-2
-3
-4
HYDROPHILIC
HYDROPHOBIC
I
II
III
IV
V
VI
VII
0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0
FRACTION OF LENGTH

FIG. 6A


Length of DNA: 2477 nts
EcoRI
400
800
1200
1600
2000
2400 nts
EcoRI
1) AatII (0)*
2) ApaI (1)
3) AccI (2)
4) AccII (0)*
5) BamHI (2)
6) AflII (1)
7) AflIII (0)*
8) AsuI (18)
9) AsuII (0)*
10) AvaI (3)
11) AvaII (6)
12) AvaIII (0)*
13) AvrII (0)*
14) AhaI (4)
15) AhaIII (0)*
16) AluI (17)
17) BamHI (2)
18) BbvI (11)
19) BclI (0)*
20) BcnI (4)

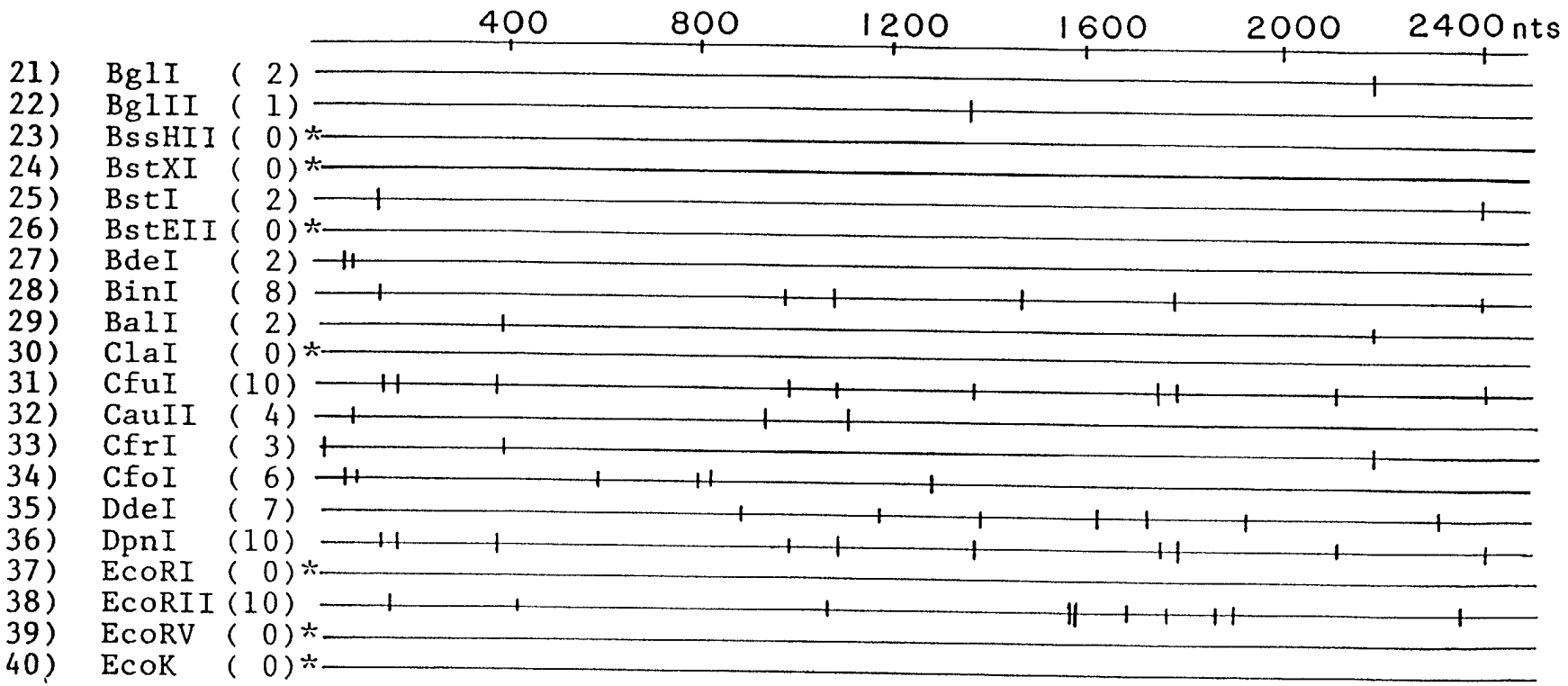

400
800
1200
1600
2000
2400 nts
21) BglI (2)
22) BglII (1)
23) BssHII (0)*
24) BstXI (0)*
25) BstI (2)
26) BstEII (0)*
27) BdeI (2)
28) BinI (8)
29) BalI (2)
30) ClaI (0)*
31) CfuI (10)
32) CauII (4)
33) CfrI (3)
34) CfoI (6)
35) DdeI (7)
36) DpnI (10)
37) EcoRI (0)*
38) EcoRII (10)
39) EcoRV (0)*
40) EcoK (0)*

FIG. 6B

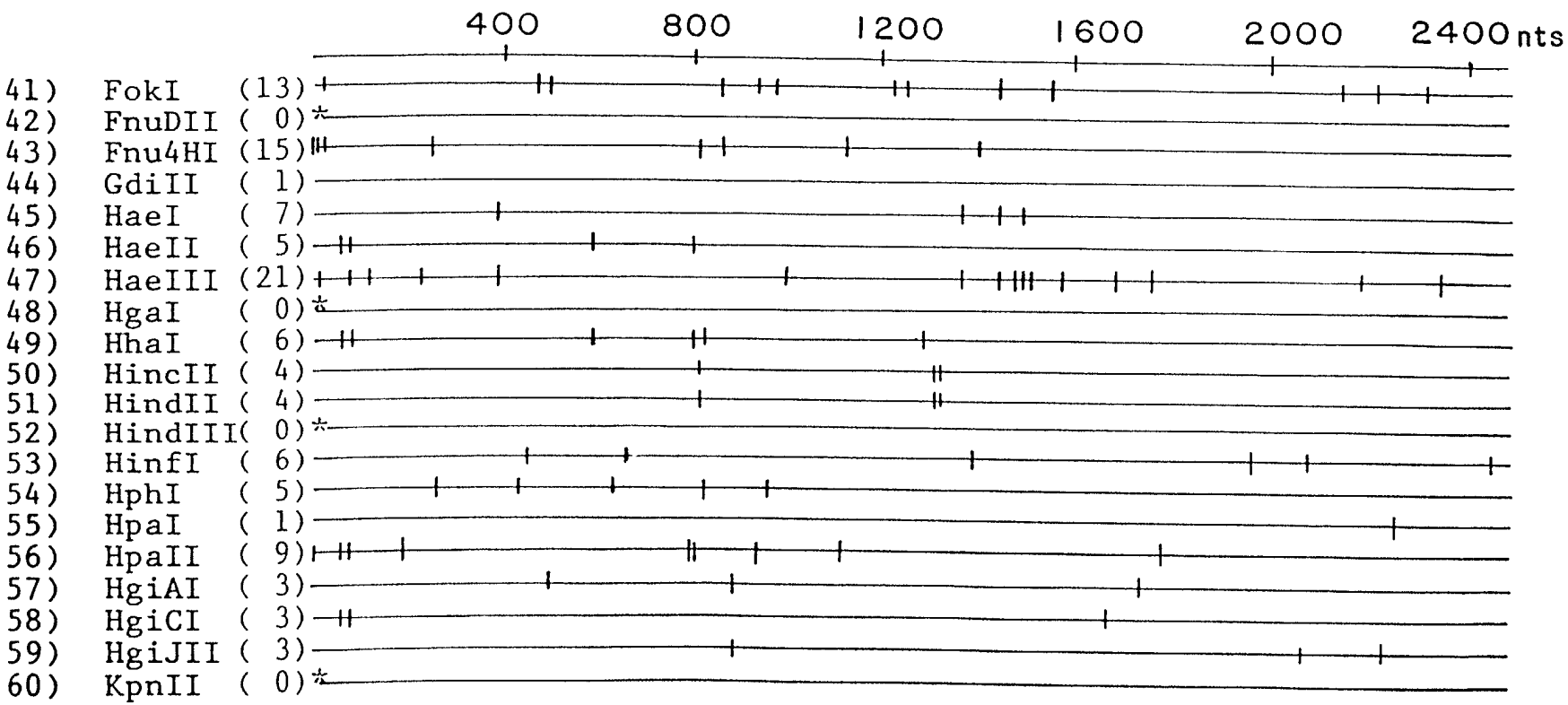

400
800
1200
1600
2000
2400 nts
41) FokI (13)
42) FnuDII (0)
43) Fnu4HI (15)
44) GdiII (1)
45) HaeI (7)
46) HaeII (5)
47) HaeIII (21)
48) HgaI (0)
49) HhaI (6)
50) HincII (4)
51) HindII (4)
52) HindIII(0)
53) HinfI (6)
54) HphI (5)
55) HpaI (1)
56) HpaII (9)
57) HgiAI (3)
58) HgiCI (3)
59) HgiJII (3)
60) KpnII (0)

FIG. 6C

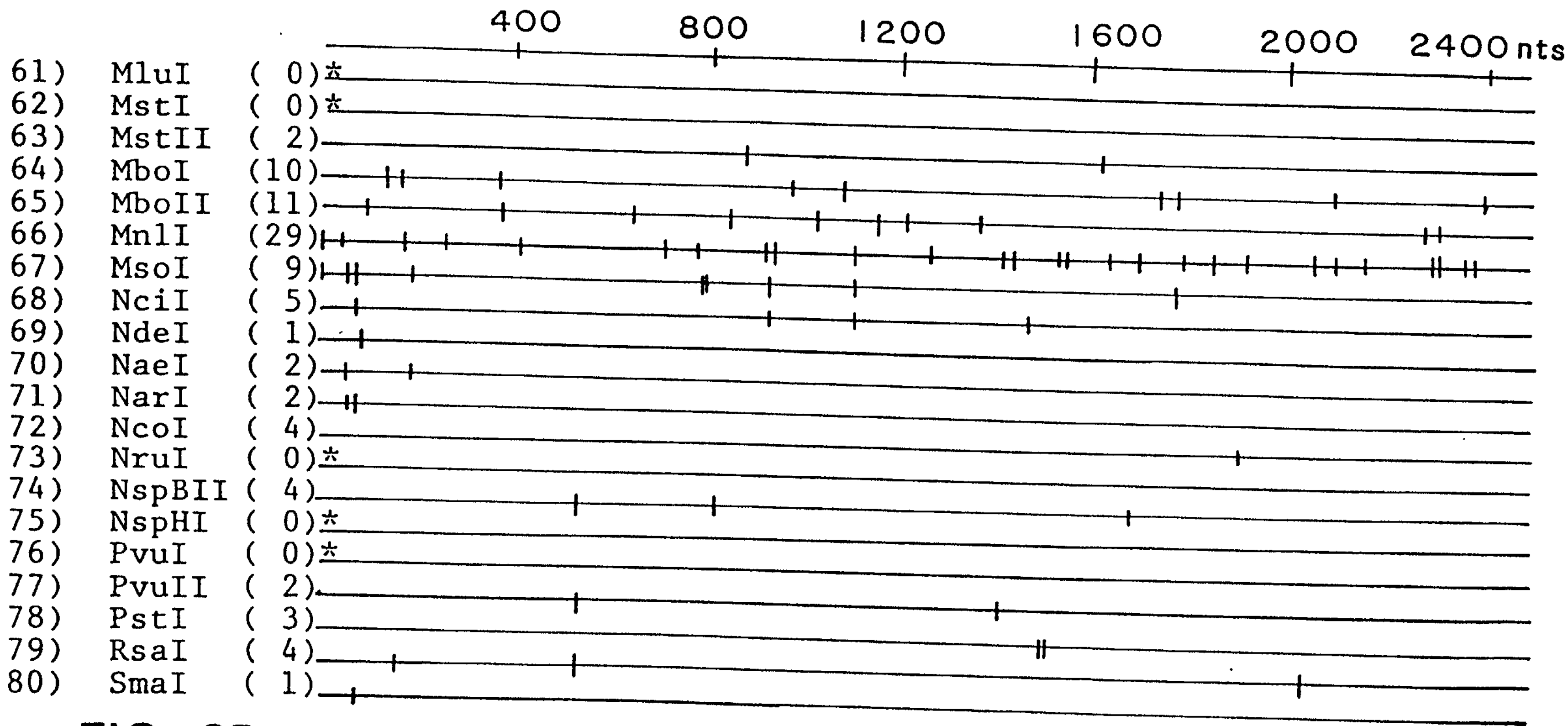

400
800
1200
1600
2000
2400 nts
61) MluI (0)*
62) MstI (0)*
63) MstII (2)
64) MboI (10)
65) MboII (11)
66) MnlI (29)
67) MsoI (9)
68) NciI (5)
69) NdeI (1)
70) NaeI (2)
71) NarI (2)
72) NcoI (4)
73) NruI (0)*
74) NspBII (4)
75) NspHI (0)*
76) PvuI (0)*
77) PvuII (2)
78) PstI (3)
79) RsaI (4)
80) SmaI (1)

FIG. 6D

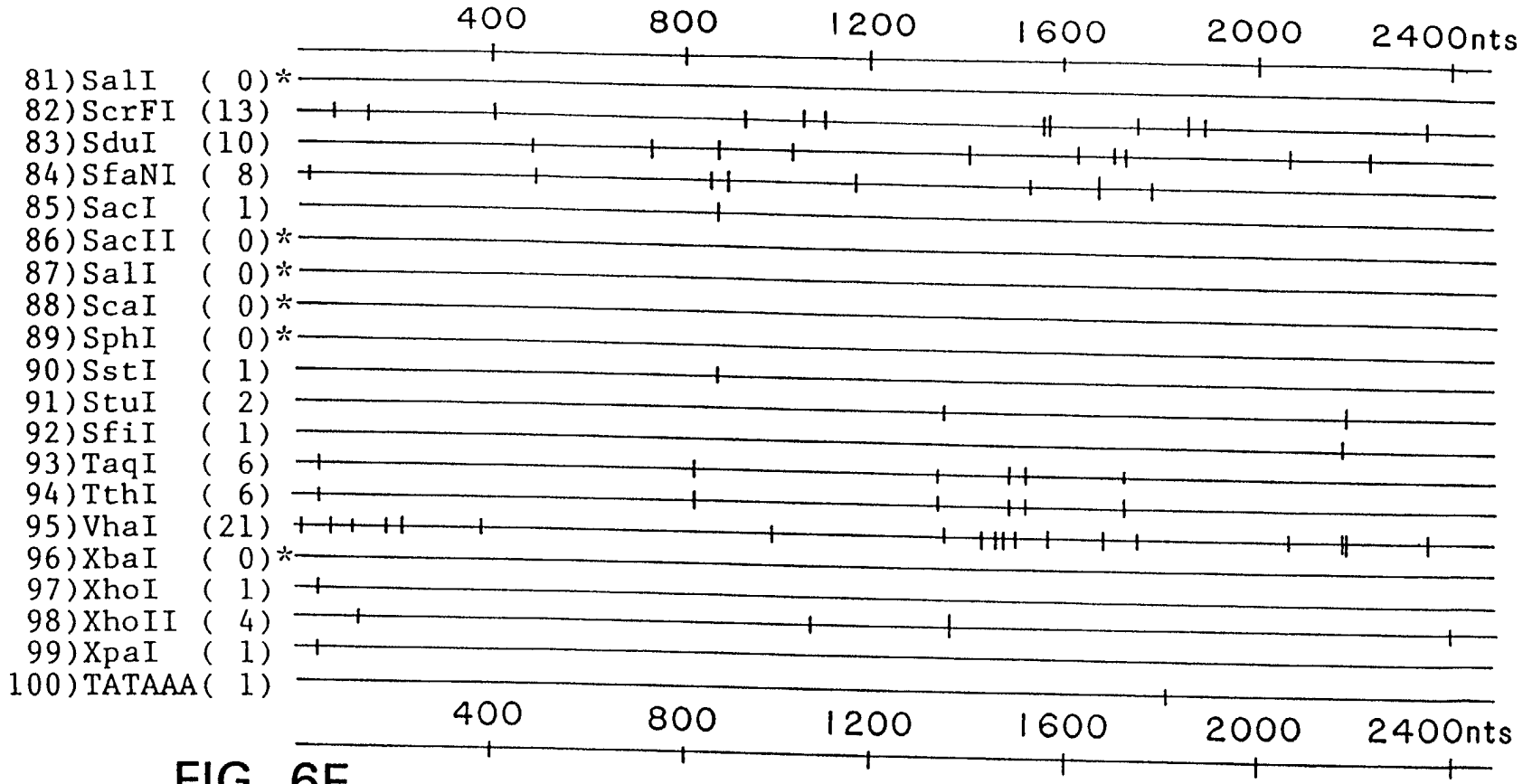


FIG. 6E

FIG. 7A

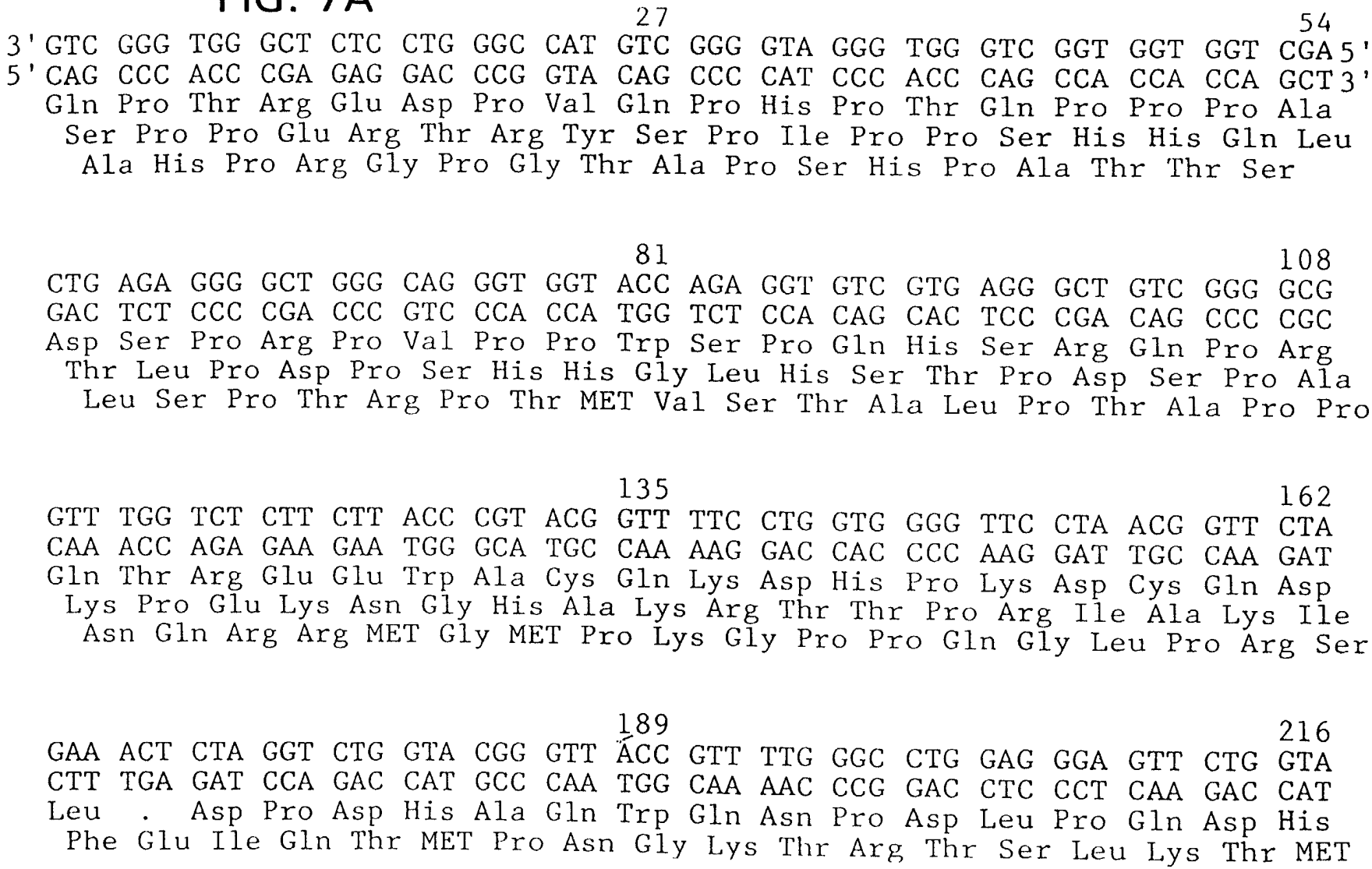


FIG. 7B

```
                                                                  243
CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT CTT TCG GTG AGT CTA CGA GCG                270
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA GAA AGC CAC TCA GAT GCT CGC
Glu Pro  .  Glu C    TT Pro Ala Glu Gly Glu Glu Ser His Ser Asp Ala Arg
 Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Lys Ala Thr Gln MET Leu Ala
  Ala Val Gly     Ser     Ser Arg Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro

                                                                  297
GTA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGA CGG GAA GAA GTA GTG TGT GTA                324
CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT
His T   Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His
 ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile
  le  Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser

                                                                  351
GGA CTT GTA TGT GAC ACT GAC GTT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG                378
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC
Pro Glu His Thr Leu  .  Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His
 Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr
   .  Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg

                                                                  405
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT                432
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln
 Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
  Gly Trp Ala MET Ser Thr Ala Pro  .  Thr Pro Ser Ser Thr Pro Pro Ser Thr
```

459 486

GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA
CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT
His . Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Leu Thr Leu Leu Pro
Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

513 540

CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG
GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC
Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
Arg Thr Ala Ala Cys Phe Pro Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

567 594

AAC GCT TGG CAC TCG TCC TTC CGG ACC CAC CTA GCC GGA GGA GAA GAT CGG GGC
TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG
Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg
Ala Asn Arg Glu Gln Glu Gly Leu Gly Gly Ser Ala Ser Ser Ser Ser Pro Gly

FIG. 7C

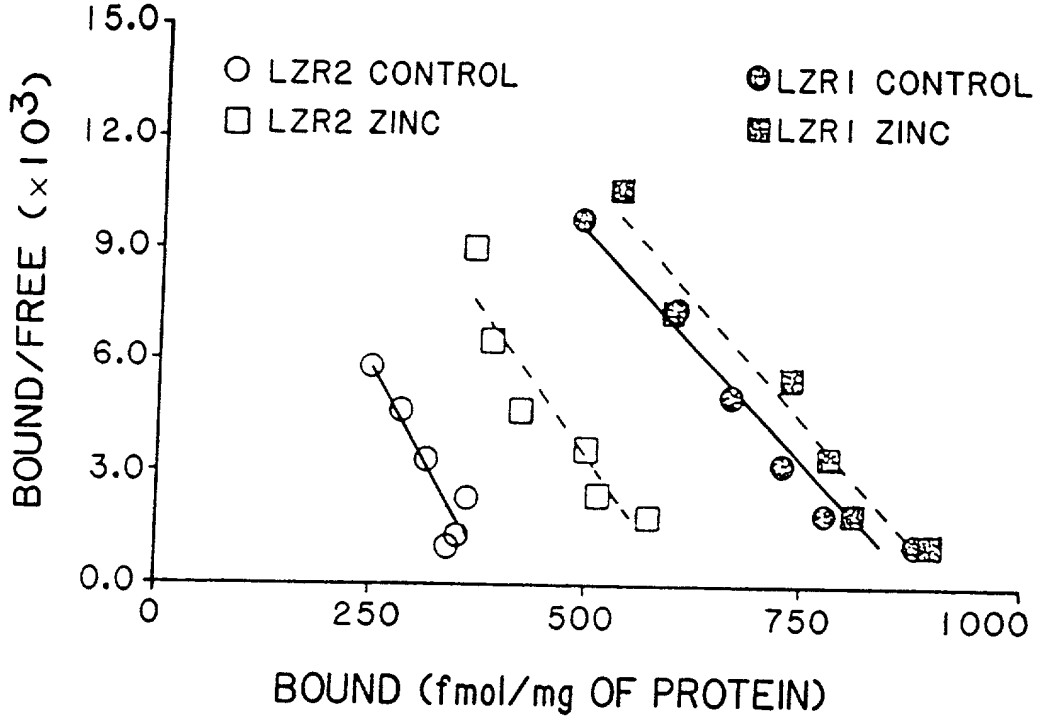

15.0
12.0
9.0
6.0
3.0
0.0
BOUND/FREE (×10³)
LZR2 CONTROL
LZR2 ZINC
LZR1 CONTROL
LZR1 ZINC
0
250
500
750
1000
BOUND (fmol/mg OF PROTEIN)

FIG. 8

FIG. 11

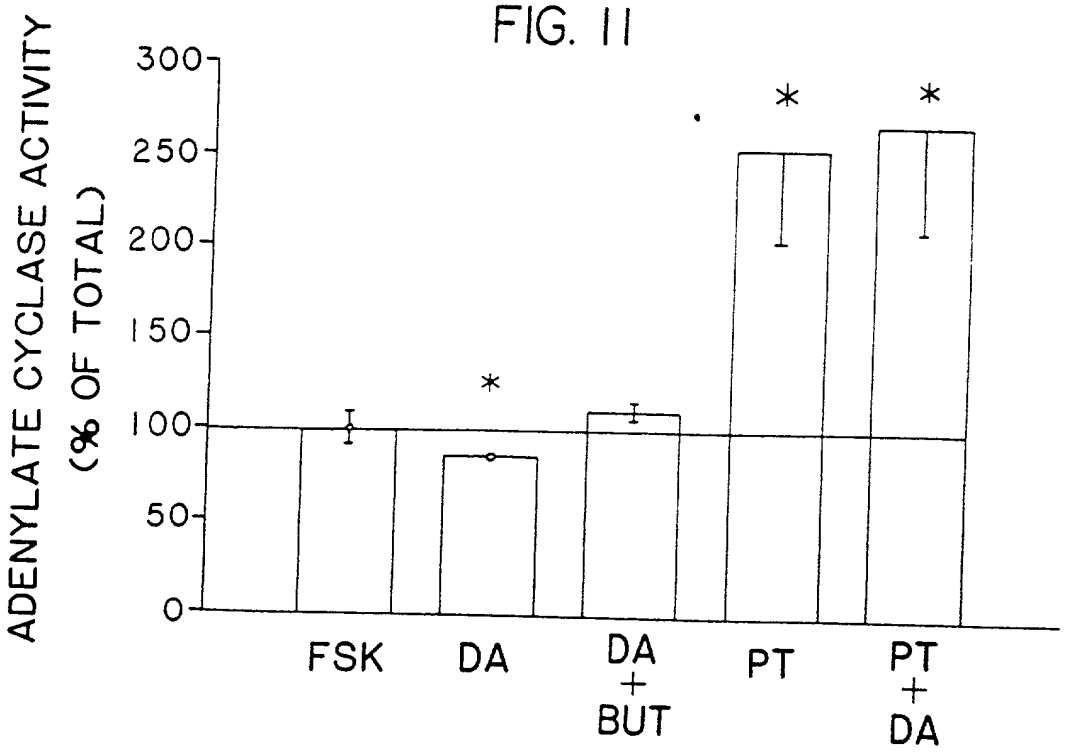

ADENYLATE CYCLASE ACTIVITY
(% OF TOTAL)
300
250
200
150
100
50
0
*
*
*
FSK
DA
DA + BUT
PT
PT + DA

FIG. 9A

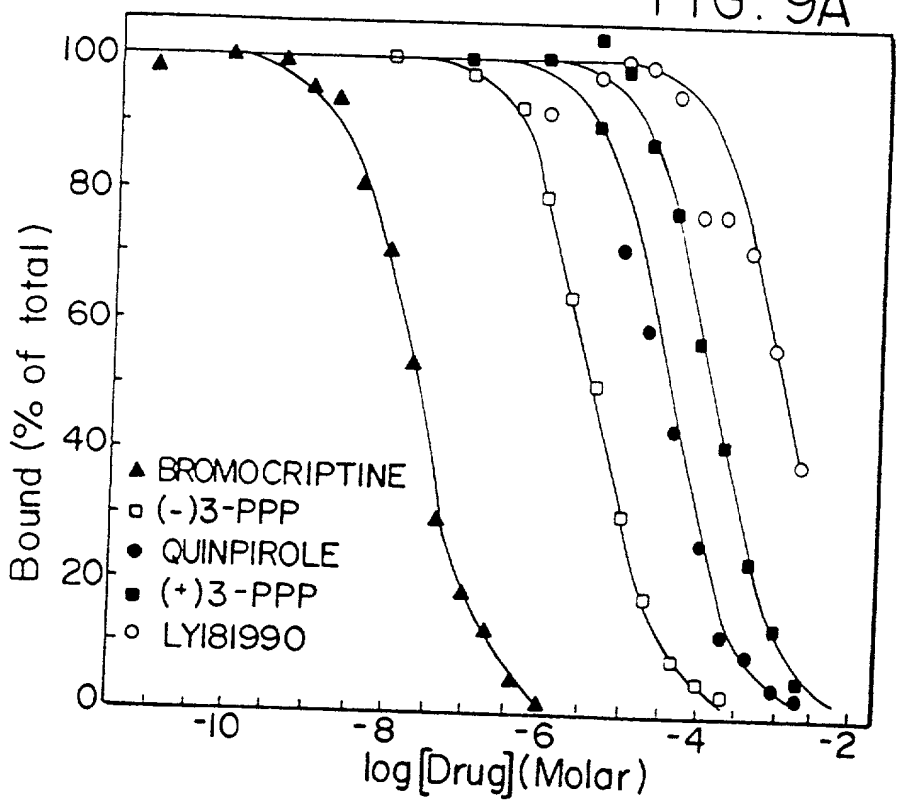
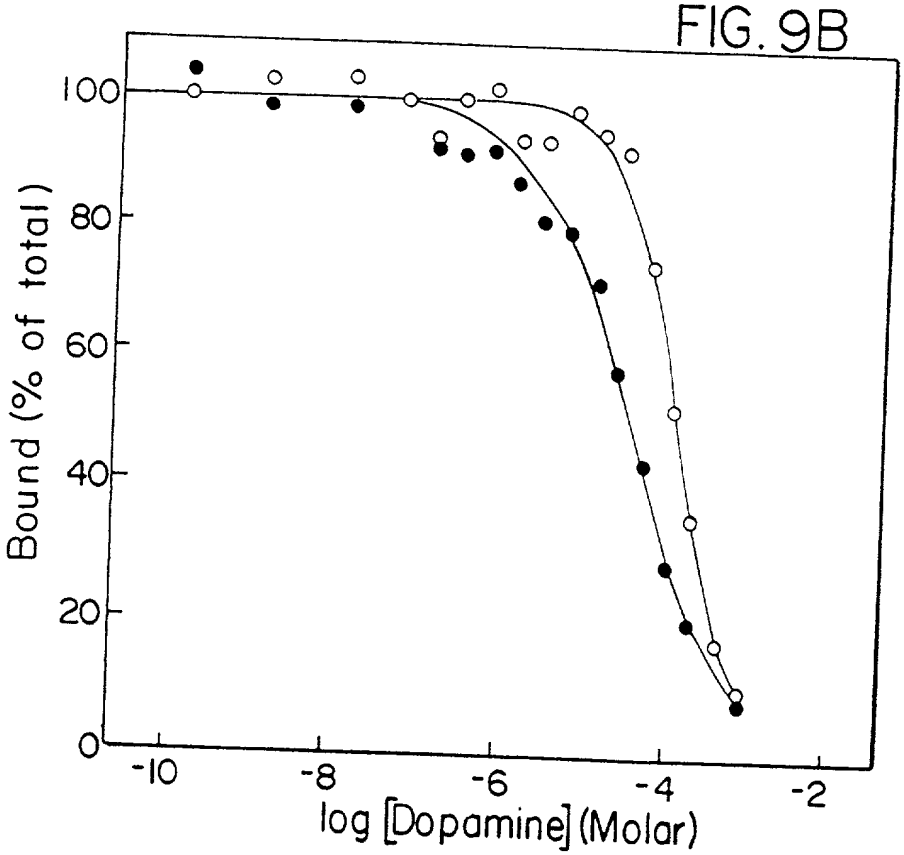

100
80
60
40
20
0
Bound (% of total)
▲ BROMOCRIPTINE
□ (-)3-PPP
● QUINPIROLE
■ (+)3-PPP
○ LY181990
-10
-8
-6
-4
-2
log [Drug] (Molar)

FIG. 9B


100
80
60
40
20
0
Bound (% of total)
-10
-8
-6
-4
-2
log [Dopamine] (Molar)

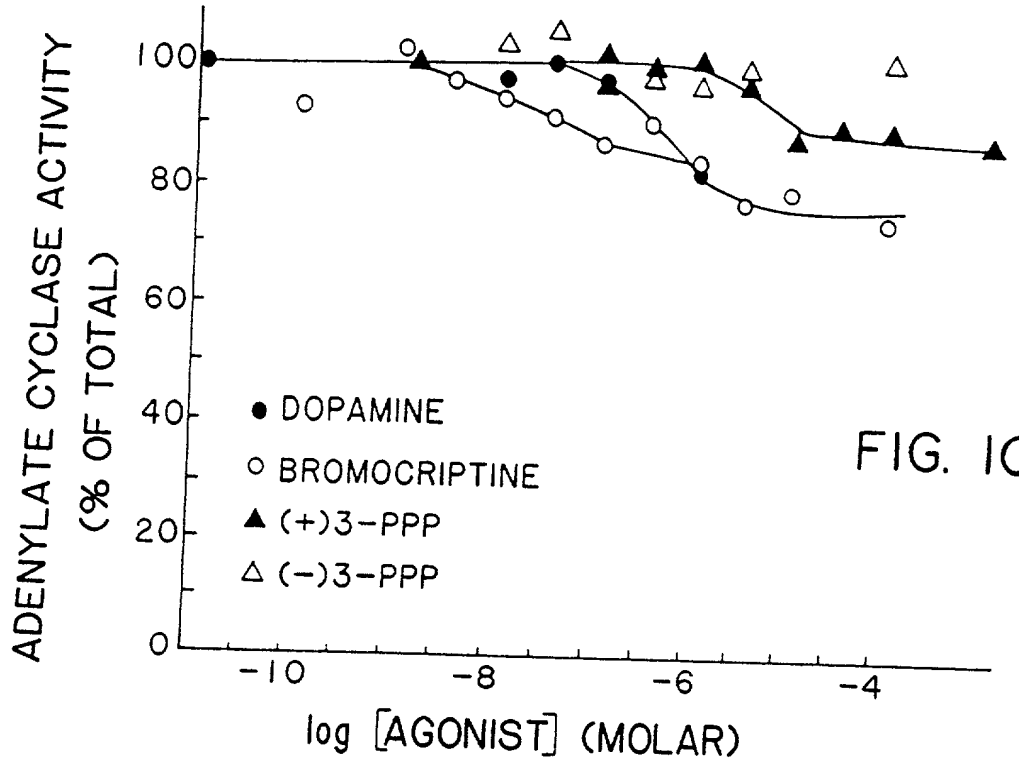


FIG. 10A

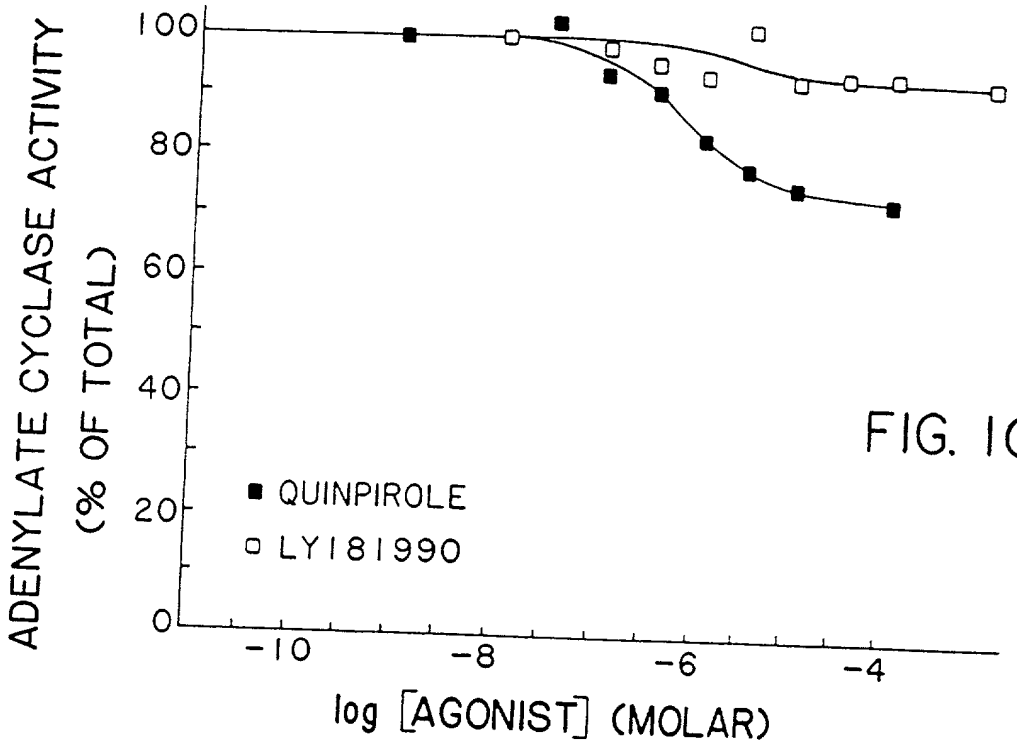


FIG. 10B

FIG. 12A

	CONTROL			+P.T.		
	BASAL	FSK	FSK+DA	BASAL	FSK	FSK+DA
$\bar{X}$	2.1	22.6	14.3	1.7	26.7	23.1
S.E.	0.2	2.2	2.1	0.4	2.0	0.5
INH	—	—	41%	—	—	14%

FIG. 12B

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
S.E.	0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
INH	—	—	53%	71%	—	—	10%	3%

FIG. 12C

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
S.E.	0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
INH	—	—	68%	88%	—	—	0%	12%

FIG. 13B-1

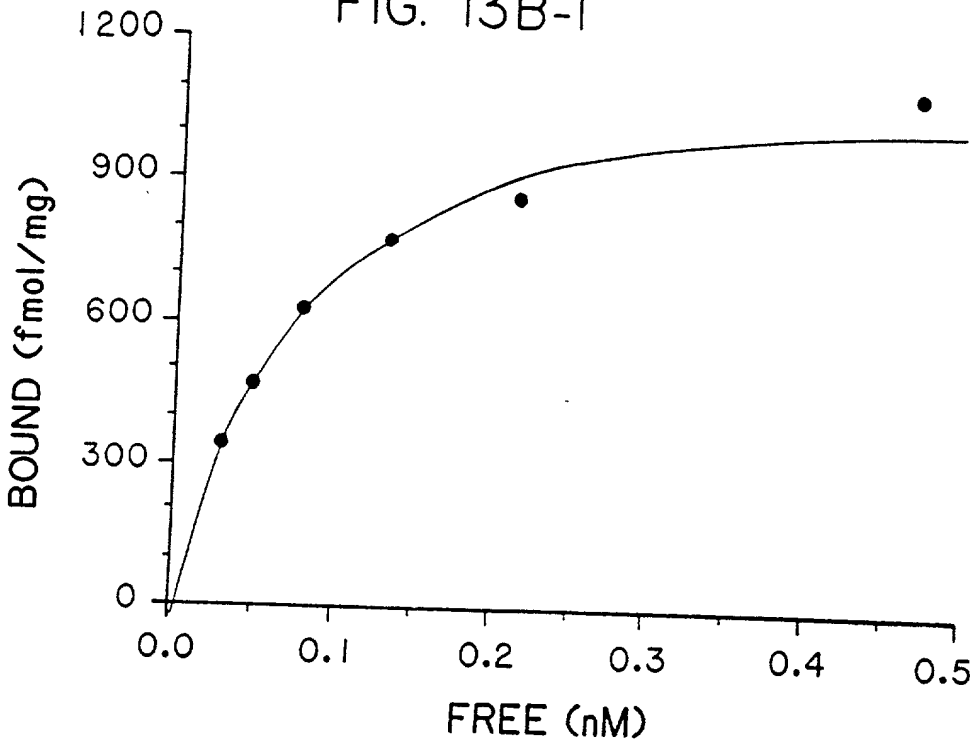


FIG. 13B-2

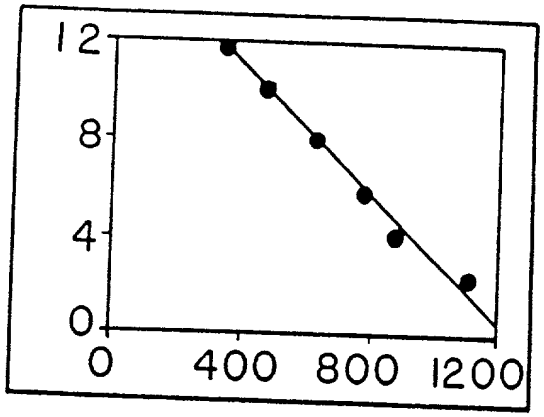
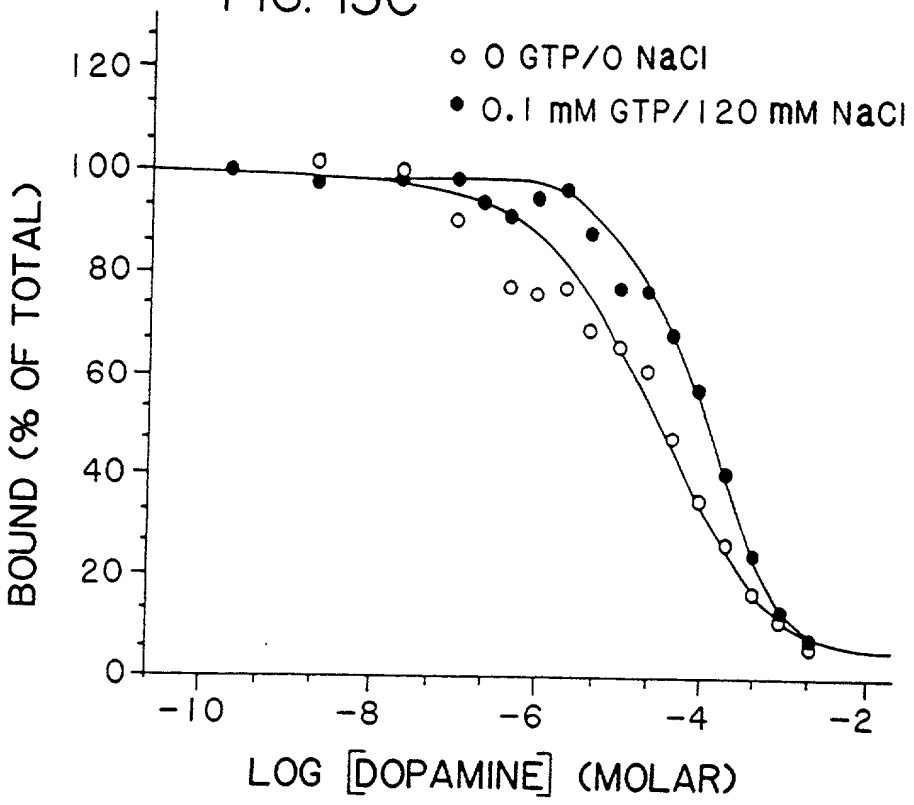


FIG. 13C



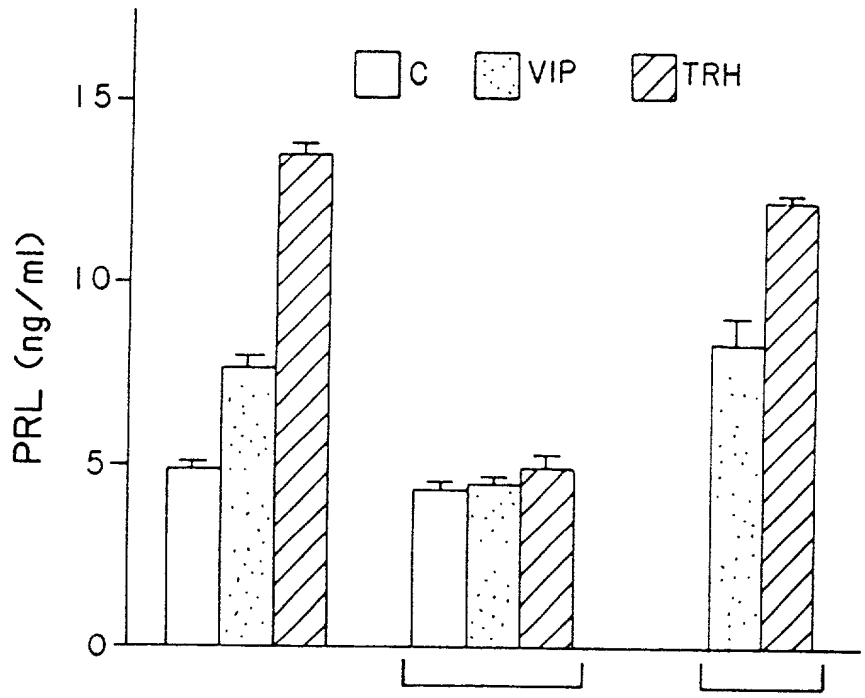


FIG. 14C

FIG.14A

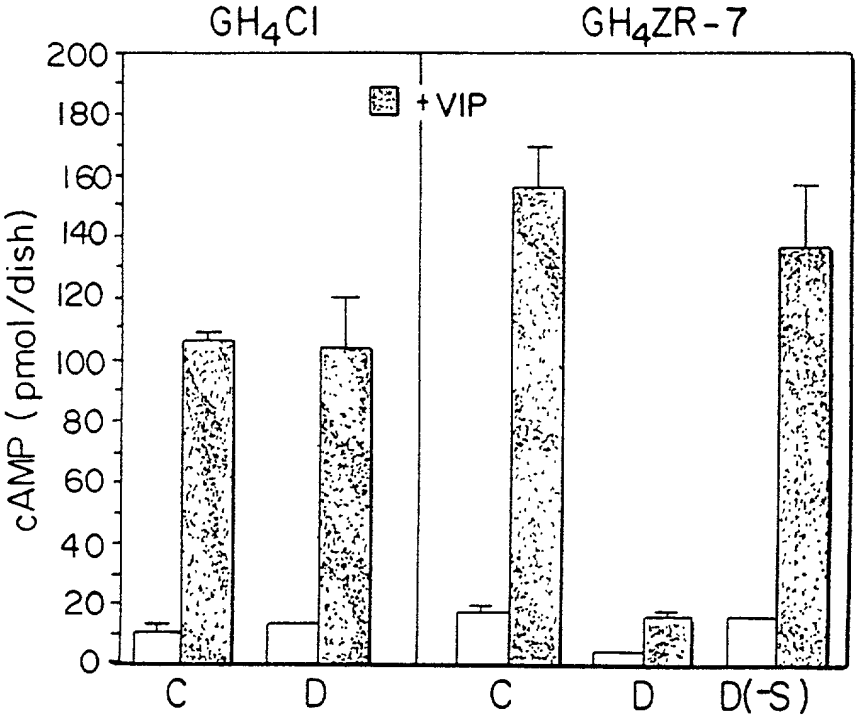


FIG.14B

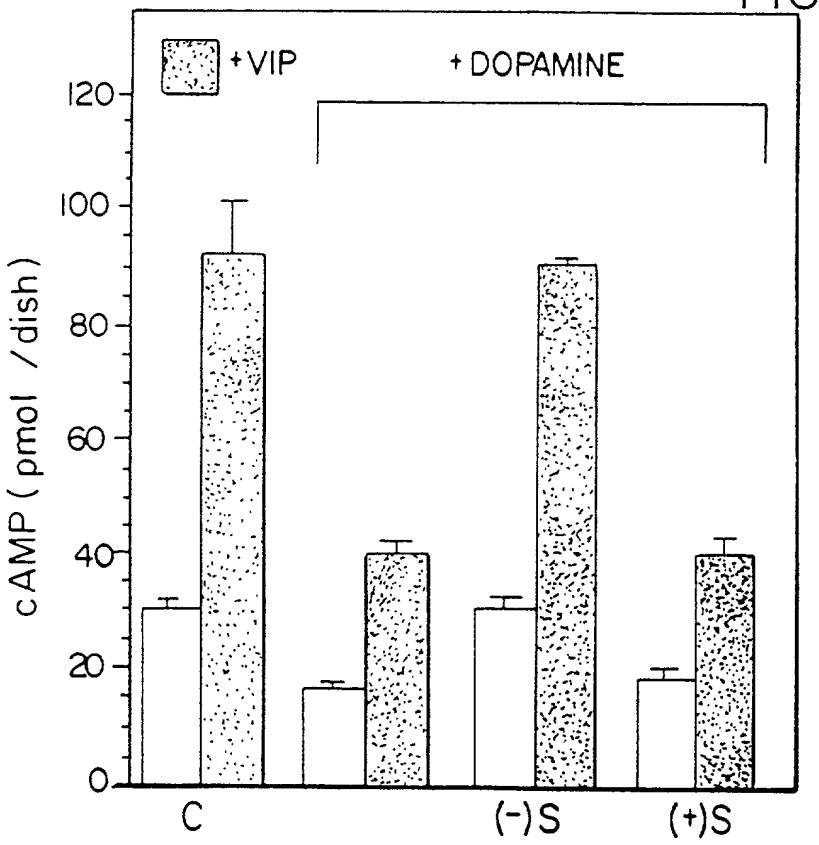


FIG. 15A

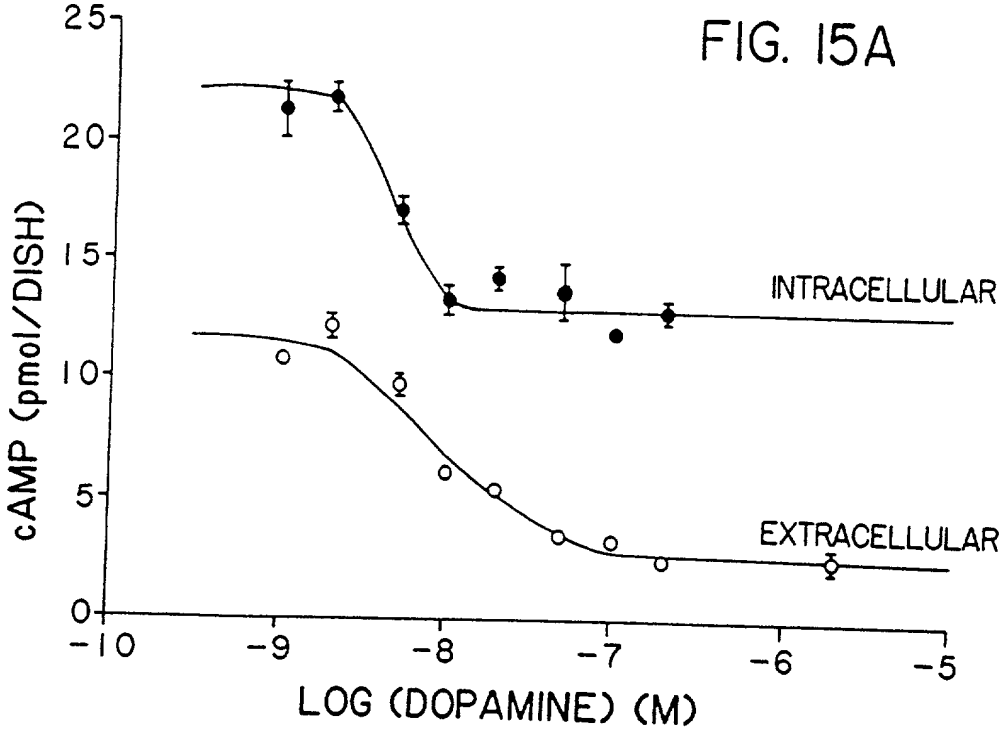
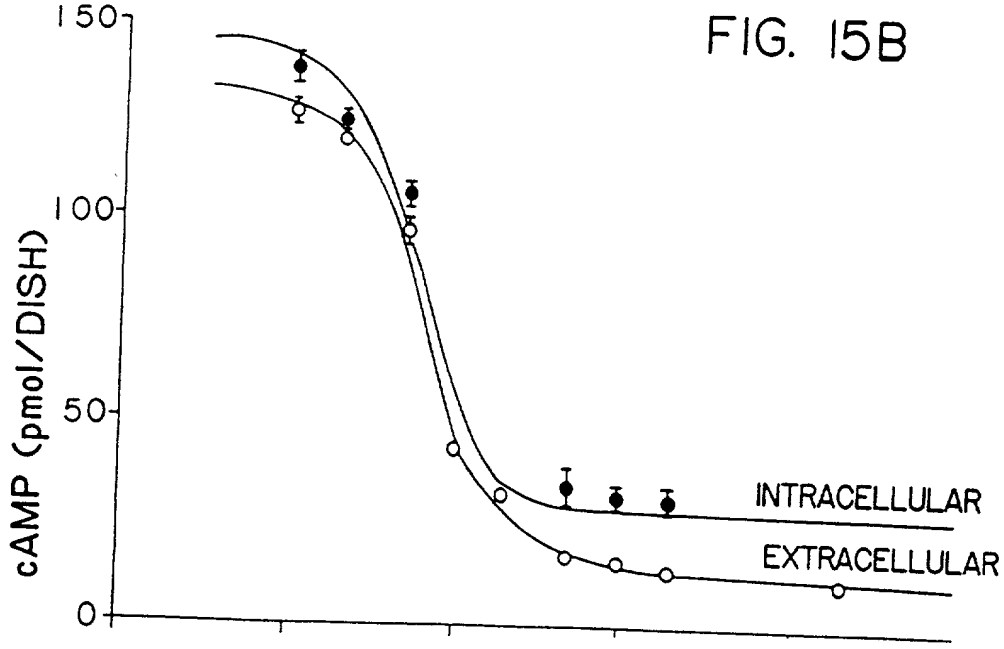


FIG. 15B



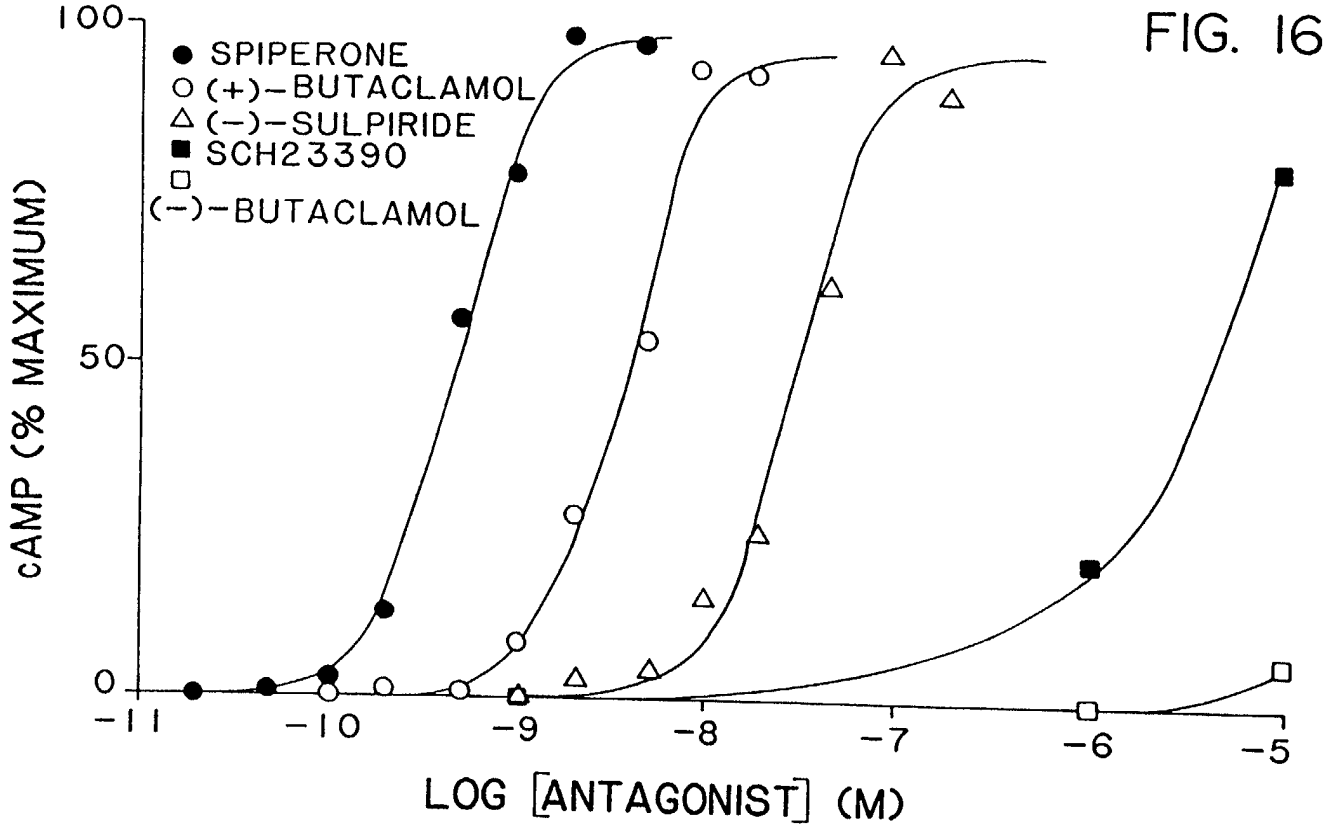


FIG. 16

FIG.17A

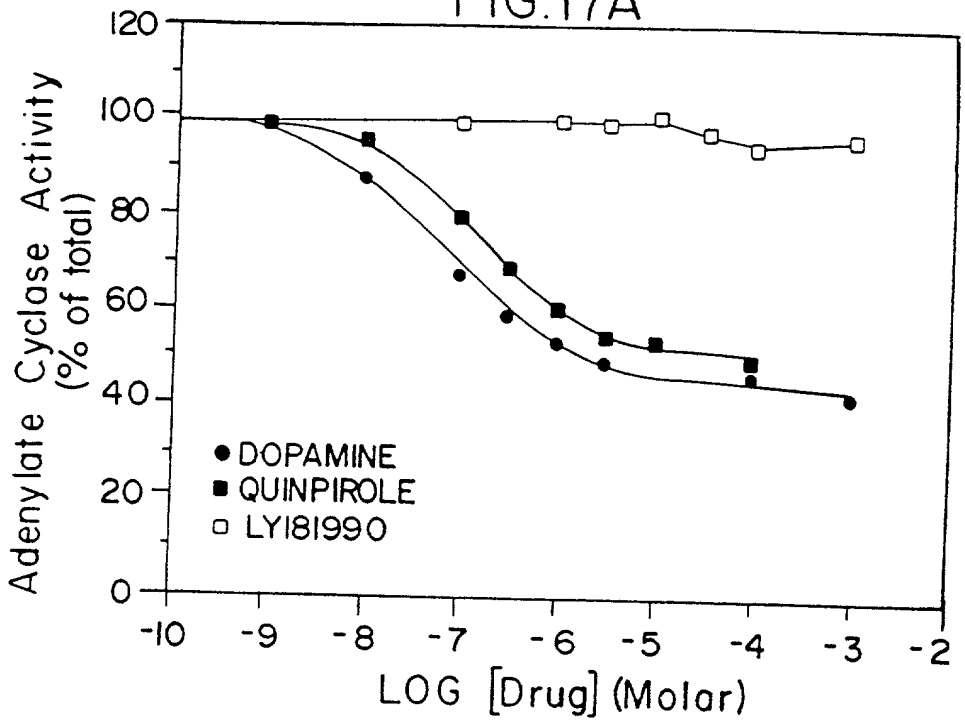
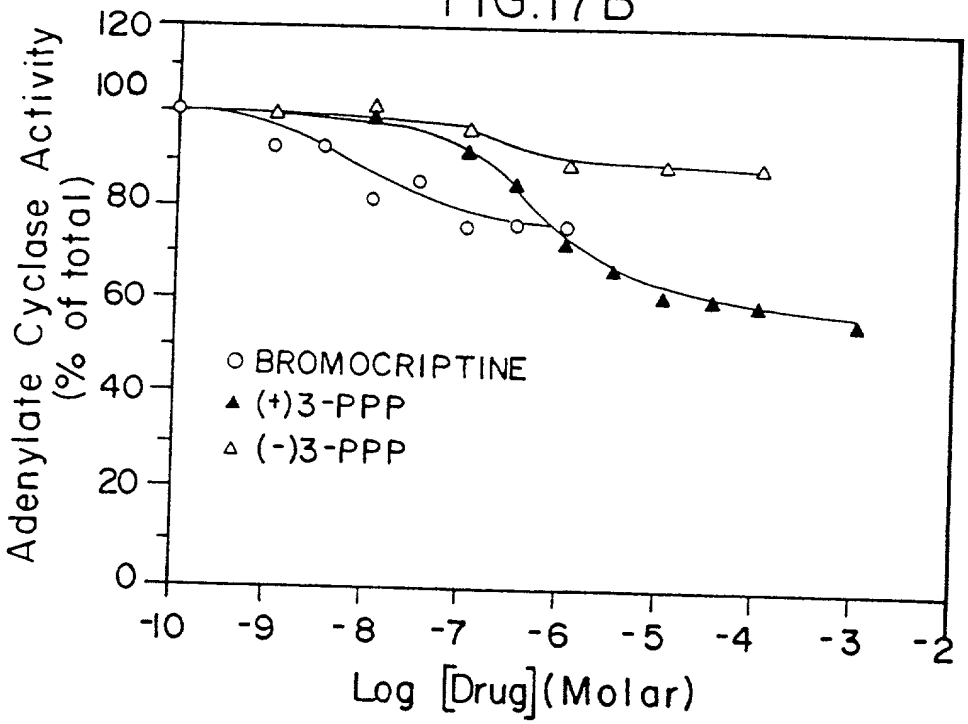


FIG.17B



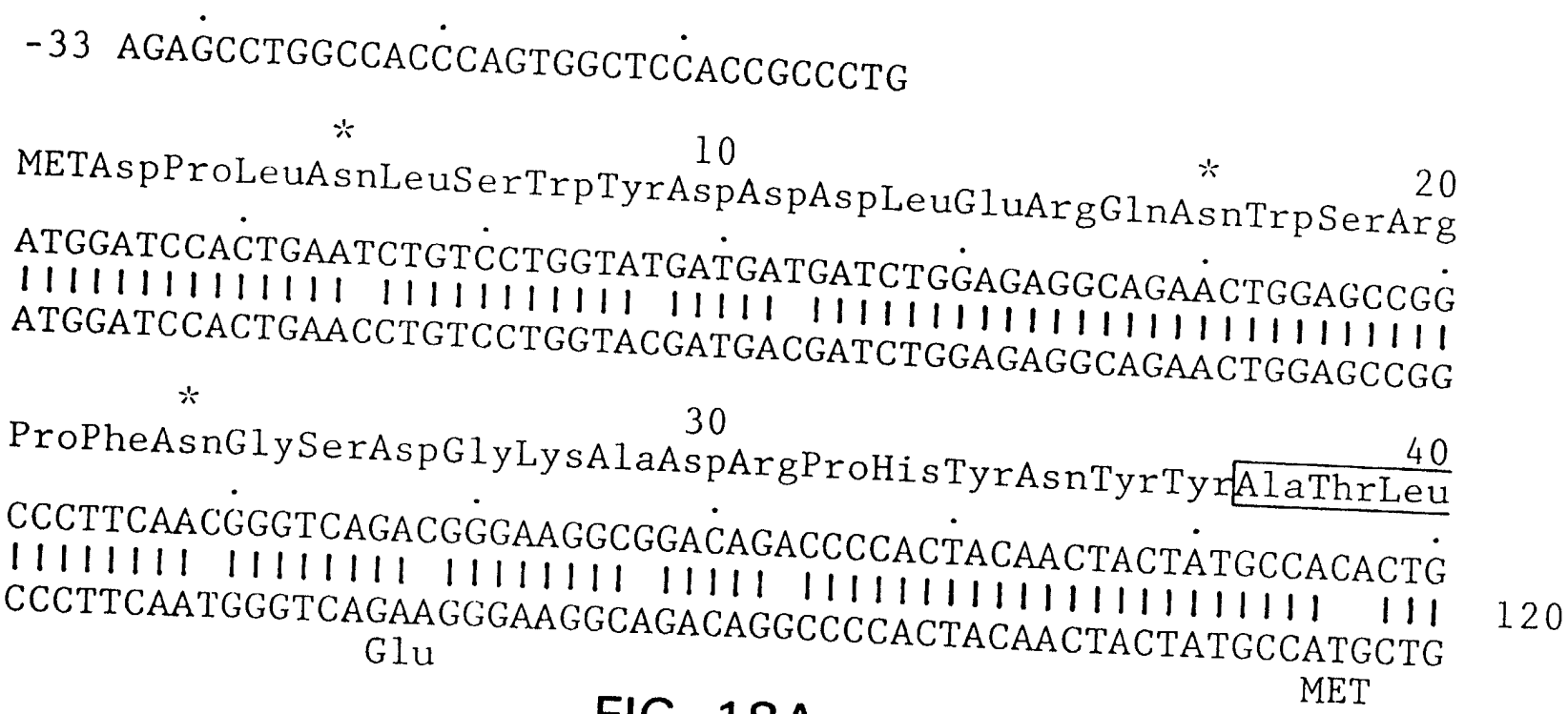

-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG
*
10
METAspProLeuAsnLeuSerTrpTyrAspAspAspLeuGluArgGlnAsnTrpSerArg
*
20
ATGGATCCACTGAATCTGTCCTGGTATGATGATGATCTGGAGAGGCAGAACTGGAGCCGG
ATGGATCCACTGAACCTGTCCTGGTACGATGACGATCTGGAGAGGCAGAACTGGAGCCGG
*
30
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu
40
CCCTTCAACGGGTCAGACGGGAAGGCGGACAGACCCCACTACAACTACTATGCCACACTG
CCCTTCAATGGGTCAGAAGGGAAGGCAGACAGGCCCCACTACAACTACTATGCCATGCTG
Glu
MET
120

FIG. 18A


LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer
CTCACCCTGCTCATCGCTGTCATCGTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC
CTCACCCTCCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC
PheIle
ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp
CGCGAGAAGGCGCTGCAGACCACCACCAACTACCTGATCGTCAGCCTCGCAGTGGCCGAC
CGAGAGAAGGCTTTGCAGACCACCACCAACTACTTGATAGTCAGCCTTGCTGTGGCTGAT
240
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp
CTCCTCGTCGCCACACTGGTCATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG
CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGGTGAGTGG

FIG. 18B

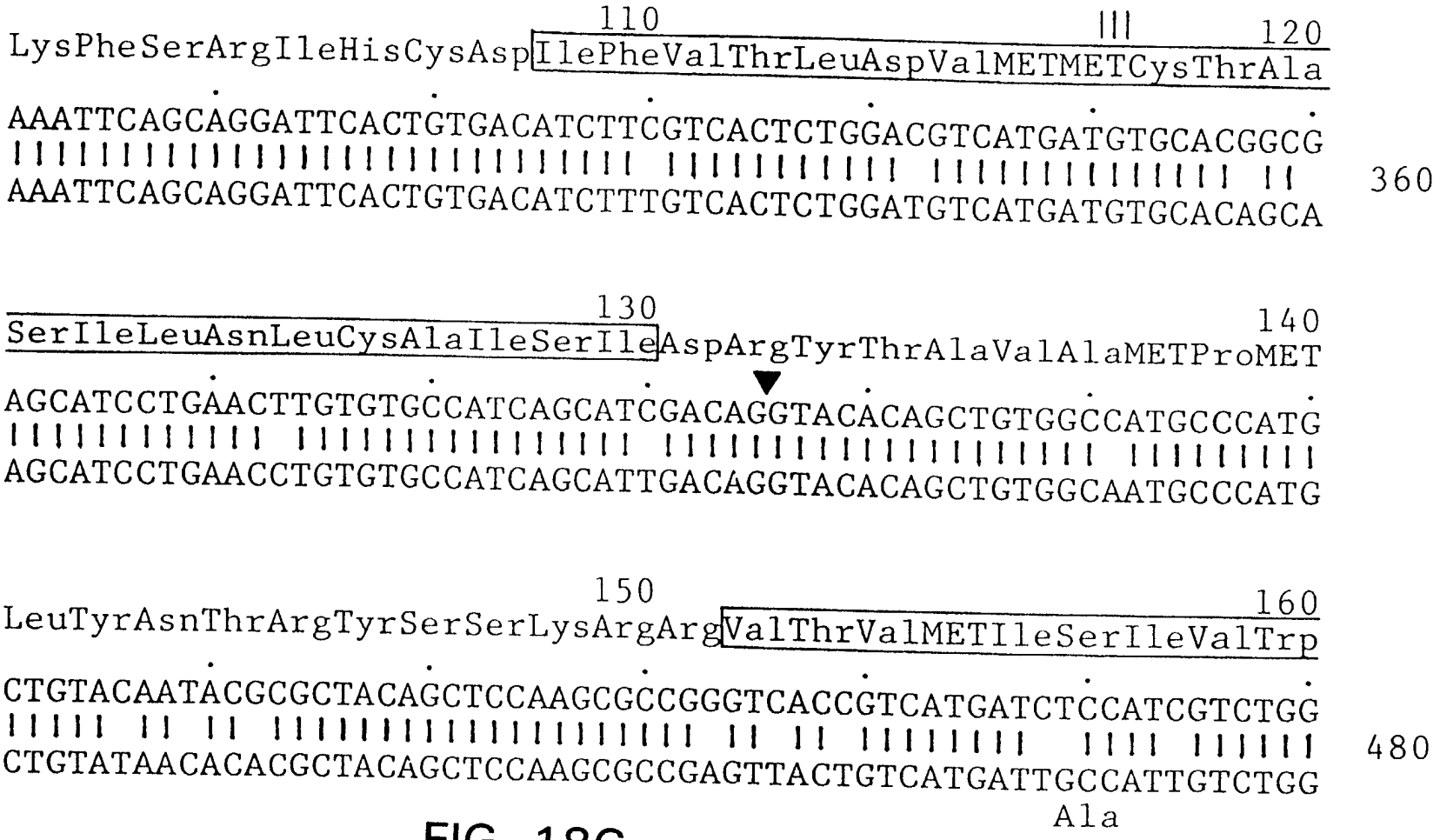

110
120
LysPheSerArgIleHisCysAspIlePheValThrLeuAspValMETMETCysThrAla
AAATTCAGCAGGATTCACTGTGACATCTTCGTCACTCTGGACGTCATGATGTGCACGGCG
AAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTGCACAGCA
360
130
140
SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET
AGCATCCTGAACTTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATG
AGCATCCTGAACCTGTGTGCCATCAGCATTGACAGGTACACAGCTGTGGCAATGCCCATG
150
160
LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp
CTGTACAATACGCGCTACAGCTCCAAGCGCCGGGTCACCGTCATGATCTCCATCGTCTGG
CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCATGATTGCCATTGTCTGG
480
Ala

FIG. 18C


IV
170
ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeu
AsnAsnAlaAspGlnAsn
180
GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAT
Thr
GluCysIleIleAlaAsn
190
V
ProAlaPheValValTyrSerSerIleValSerPheTyrVal
200
GAGTGCATCATTGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
GAGTGTATCATTGCCAACCCTGCCTTTGTGGTCTACTCCTCCATTGTCTCATTCTACGTG
600
ProPheIleValThrLeuLeuValTyrIle
210
LysIleTyrIleValLeuArgArgArgArg
220
CCCTTCATTGTCACCCTGCTGGTCTACATCAAGATCTACATTGTCCTCCGCAGACGCCGC
CCCTTCATCGTCACTCTGCTGGTCTATATCAAAATCTACATCGTCCTCCGGAAGCGCCGG
Lys

FIG. 18D

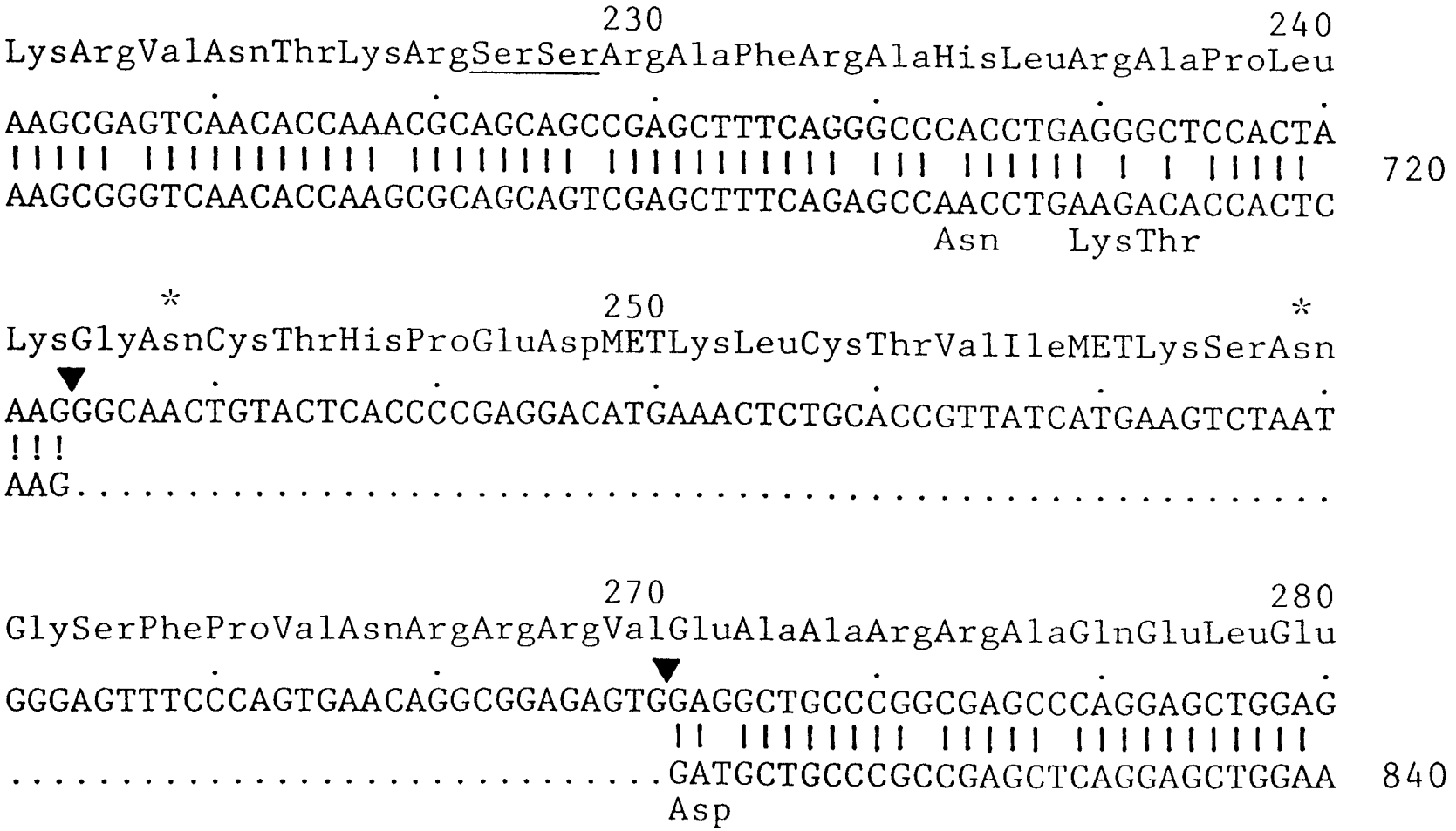


FIG. 18E

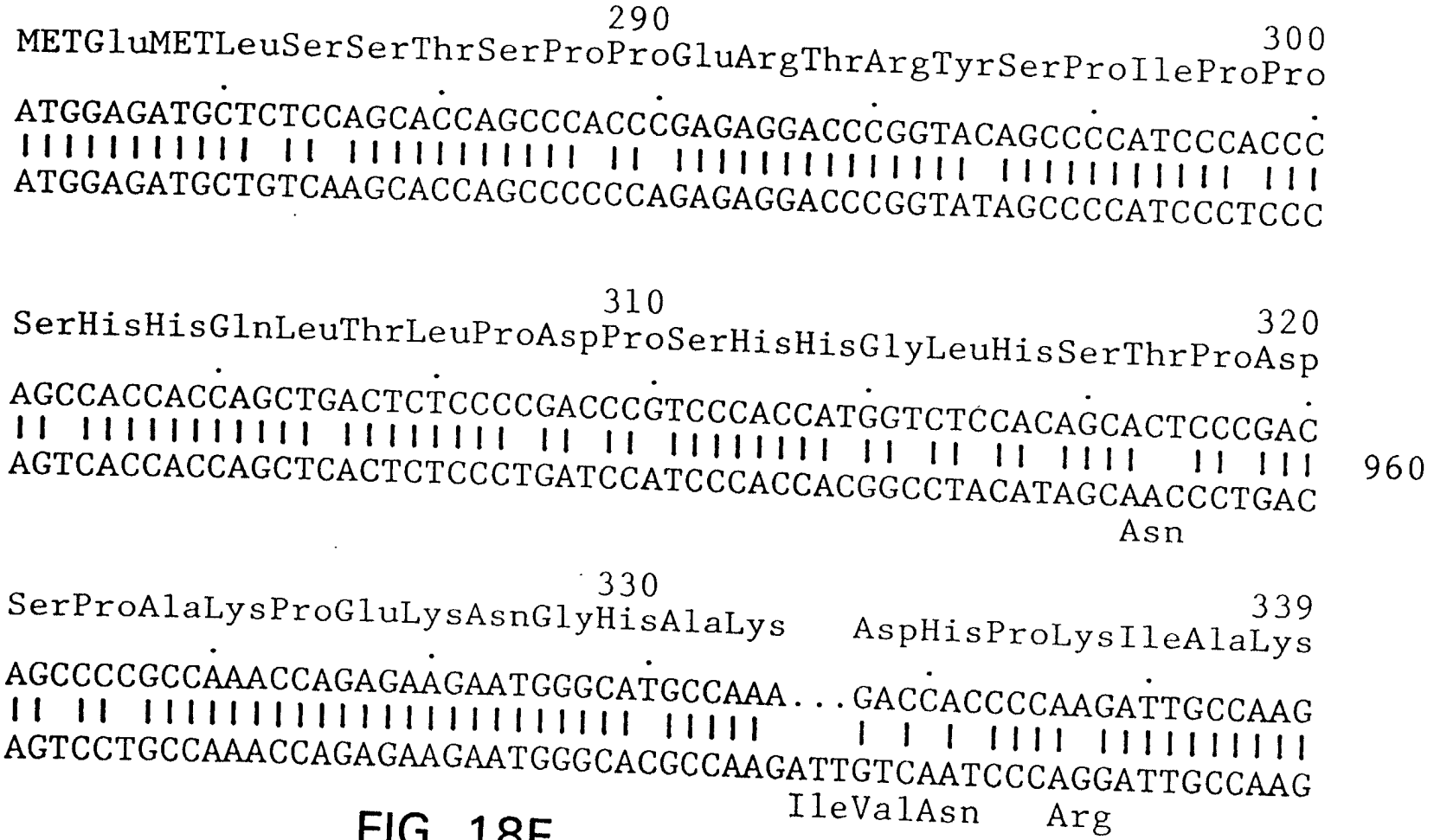

290
METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro
ATGGAGATGCTCTCCAGCACCAGCCCACCCGAGAGGACCCGGTACAGCCCCATCCCACCC
ATGGAGATGCTGTCAAGCACCAGCCCCCCAGAGAGGACCCGGTATAGCCCCATCCCTCCC
310
320
SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp
AGCCACCACCAGCTGACTCTCCCCGACCCGTCCCACCATGGTCTCCACAGCACTCCCGAC
AGTCACCACCAGCTCACTCTCCCTGATCCATCCCACCACGGCCTACATAGCAACCCTGAC
960
Asn
330
339
SerProAlaLysProGluLysAsnGlyHisAlaLys
AspHisProLysIleAlaLys
AGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAA...GACCACCCCAAGATTGCCAAG
AGTCCTGCCAAACCAGAGAAGAATGGGCACGCCAAGATTGTCAATCCCAGGATTGCCAAG
IleValAsn
Arg

FIG. 18F

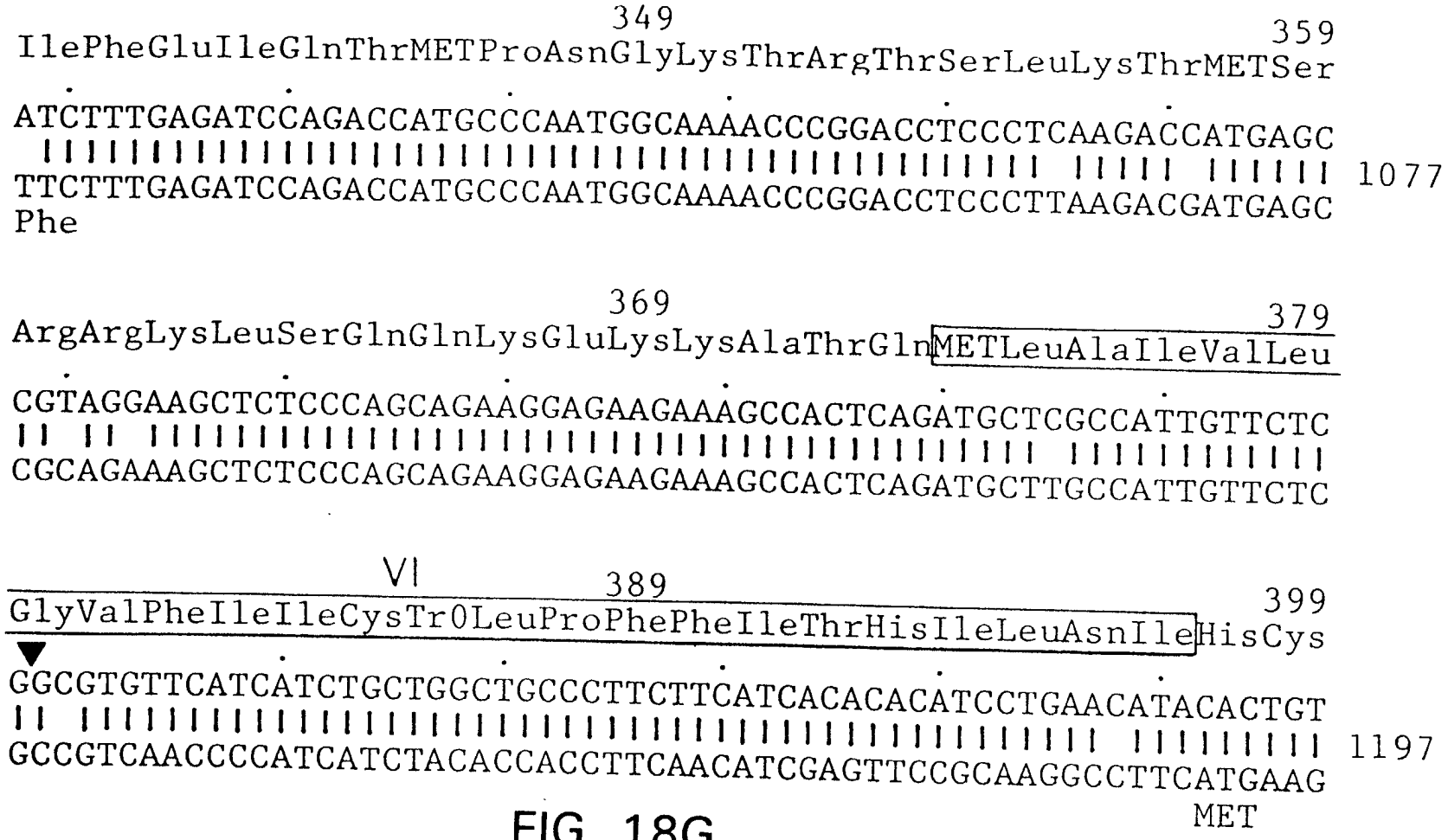

349
359
IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
ATCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTCAAGACCATGAGC
TTCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTTAAGACGATGAGC
1077
Phe
369
379
ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGlnMETLeuAlaIleValLeu
CGTAGGAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTCGCCATTGTTCTC
CGCAGAAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTTGCCATTGTTCTC
VI
389
399
GlyValPheIleIleCysTr0LeuProPhePheIleThrHisIleLeuAsnIleHisCys
GGCGTGTTCATCATCTGCTGGCTGCCCTTCTTCATCACACACATCCTGAACATACACTGT
GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
1197
MET

FIG. 18G

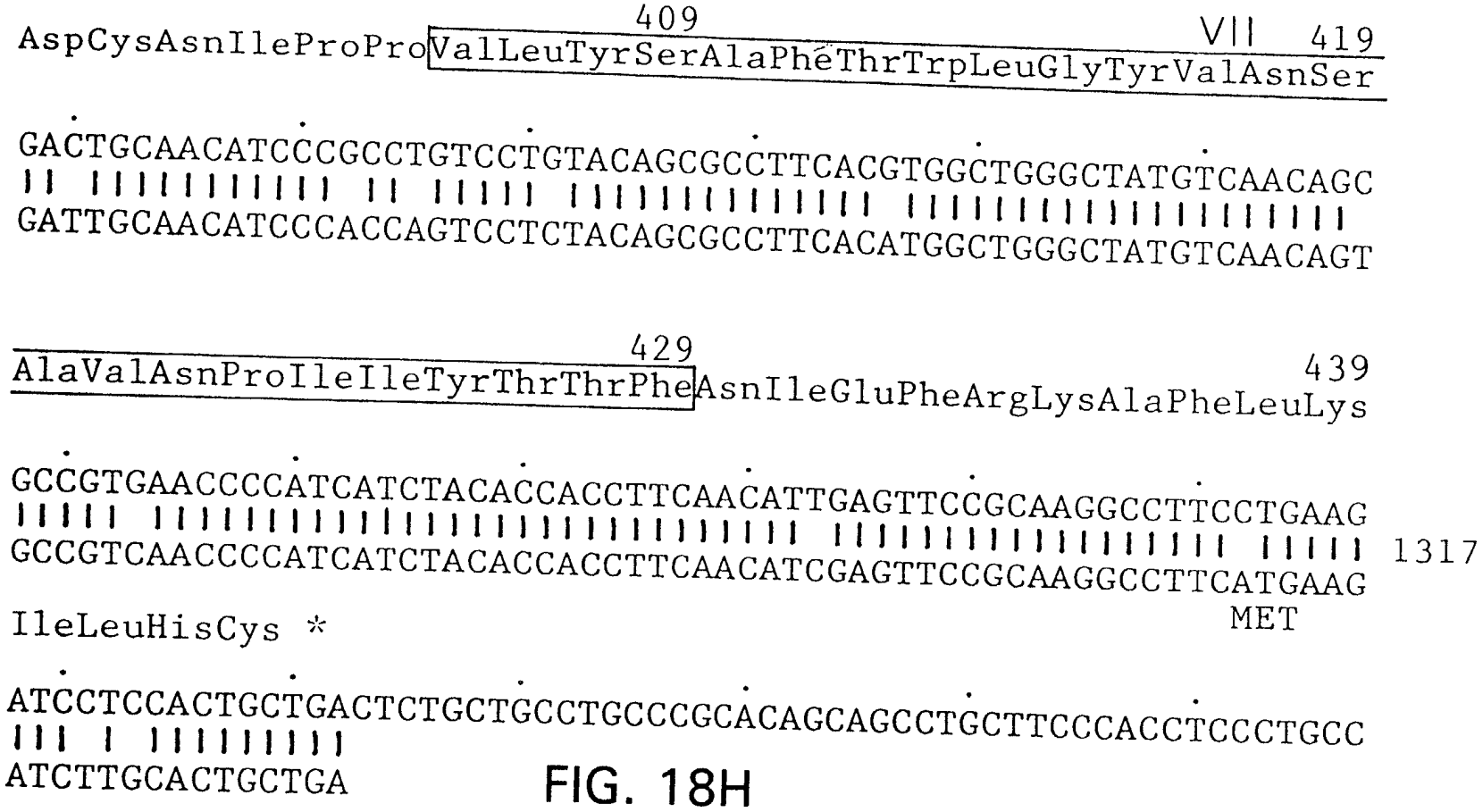


FIG. 18H

CAGGCCGGCCAGCCTCACCCTTGCGAACCGTGAGCAGGAAGGCCTGGGTGGATCGGCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG

CACACCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557

GGCCCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCCACCTCCAGTCCCCCTATCCTT

GGCACCAAAGATGCAGCCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCCAGAGGCTGAGTTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGGCGGT

GGGGAGAGATGGACAGTTCACACCCTGCAAGGCCCACAGGAGGCAAGCAAGCTCTCTTGC 1797

CGAGGAGCCAGGCAACTTCAGTCCTGGGAGACCCATGTAAATACCAGACTGCAGGTTGGA

CCCCAAGGATTCCCAAGCCAAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTTCCACAT

GCTCTGAGAAGAGGAGCCCTCATCTTGAAGGGCCCAGGAGGGTCTATGGGGAGAGGAACT 2037

CCTTGGCCTAGCCCACCCTGCTGCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC

ACATGCTGGCCAGCCTGGGGCCTGGCAGGGAGGTCAGGCCCTGGAACTCTATCTGGGCCT 2157

GGGCTAGGGACATCAGAGGTTCTTTGAGGGACTGCCTCTGCCACACTCTGACGCAAAACC

ACTTTCCTTTTCTATTCCTTCTGGCCTTTCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277

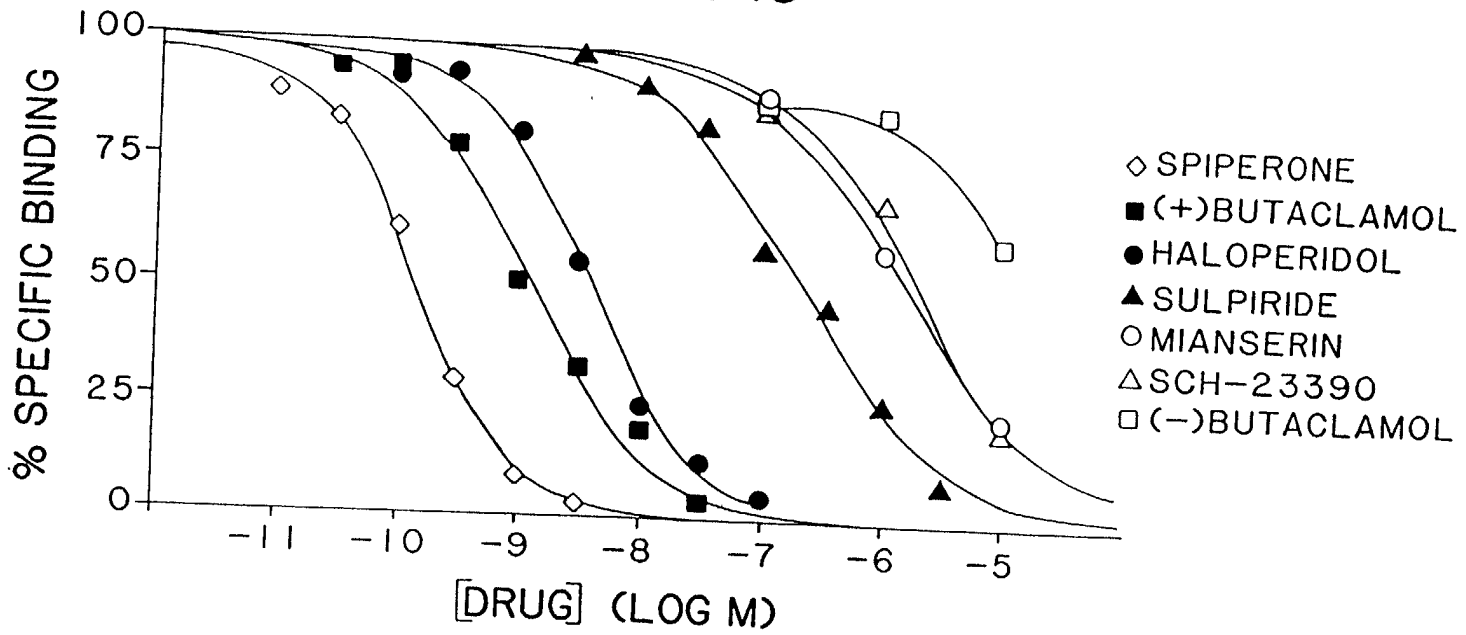
CTCTGCCTTAGAGGAGCCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC

CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGGCCTAGACTCTG 2397

TAACATCACTATCCGATGCACCAAACTAATAAAACTTTGACGAGTCACCTTC $(A)_n$ 2449

FIG. 18J

FIG. 19



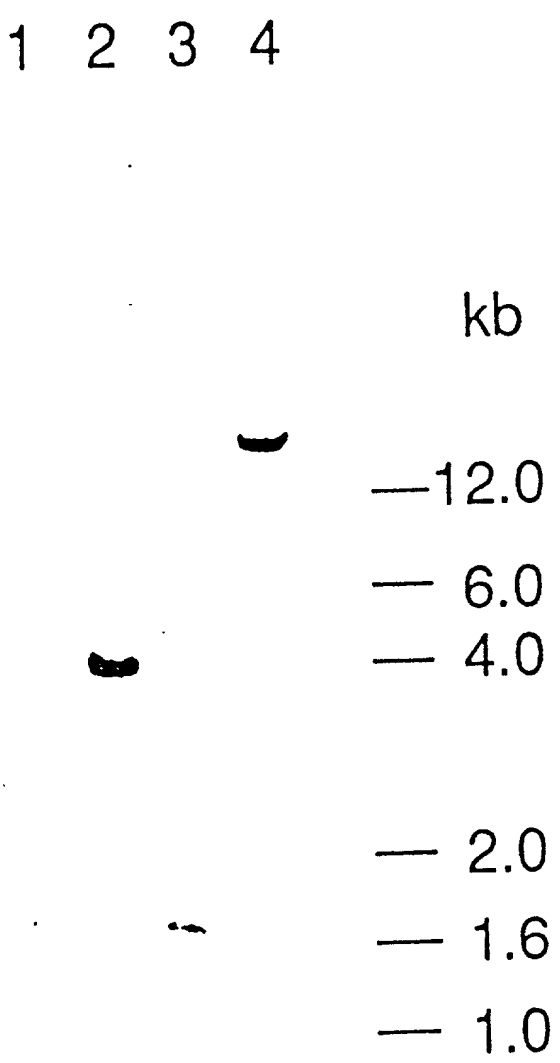
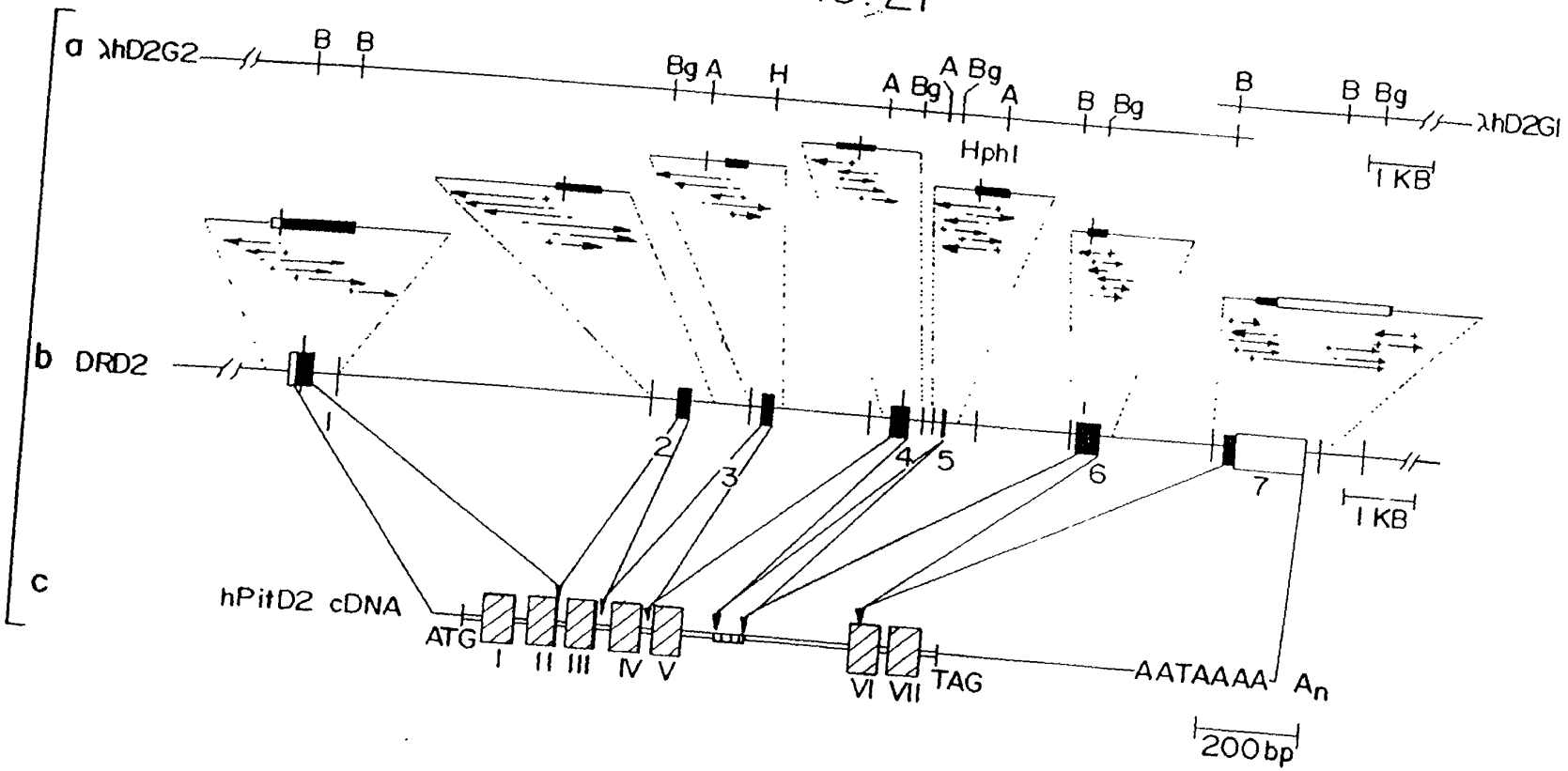


FIG. 20

FIG. 21



DRUG	HUMAN D_2	RAT D_2	RAT STRIATUM
SPIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (D1)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [^{3}H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22